STIC-Biotech/ChemLib

79094

①   ②

Please search the sequences in Application 09/910,186 against 08/123,975;   60146,192;   60/133,866; 60/133868;   60/133869;   60/133,865;   60133,873 and   60/133,867. Thanks

Ginny Portner
CM1, Art Unit 1645
Room 7e13
Mail box 7e12
(703) 308-7543

Ginny,
     None of the provisional cases have CRF's, so
I could only compare ① with ②.
        Barb

RECEIVED OCT 30 2002

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: _BoB_
Phone: _____
Location: _____
Date Picked Up: _11-7_
Date Completed: _11-7-02_
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _/_

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

```
> O <
O| /O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-910-186a-1.res made by bobryen on Thu 7 Nov 102 14:39:29-PST.

Query sequence being compared:US-09-910-186A-1 (1-1332)
Number of sequences searched:                3
Number of scores above cutoff:               3

Results of the initial comparison of US-09-910-186A-1 (1-1332) with:
        File :US08123975A.seq
```

```
100-
      :
    N :
    U 50-
    M :
    B :
    E :
    R :
      :
    O 10-
    F :
      :
    S :
    E 5-
    Q :
    U :
    E :
    N :
    C :
    E :
    S :
      0---------------------------------------------------------------------
SCORE 0  146  291  437  583  728  874  1020  1165  1311
STDEV    -1   -1                      0

              PARAMETERS

Similarity matrix   Unitary
Mismatch penalty    1
Gap penalty         5.00
Gap size penalty    0.33
Cutoff score        1
Randomization group 0

        K-tuple         4
        Joining penalty 30
        Window size     500

              SEARCH STATISTICS

Scores:    Mean     Median    Standard Deviation
           1053     539       446.29

Times:     CPU                Total Elapsed
           00:00:00.00        00:00:00.00

Number of residues:             4027
Number of sequences searched:   3
Number of scores above cutoff:  3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                                               Init.  Opt.
Sequence Name    Description                            Length  Score  Score  Sig.  Frame
------------------------------------------------------------------------------------------
1. US-08-123-975A-4  Sequence 4, Application U          1338    1311   1314   0.58    0
2. US-08-123-975A-1  Sequence 1, Application U          1338    1311   1314   0.58    0
                     **** 1 standard deviation below mean ****
3. US-08-123-975A-6  Sequence 6, Application U          1351    538    704   -1.15    0


1. US-09-910-186A-1 (1-1332)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =  1311    Optimized Score     =  1314   Significance  =  0.58
Residue Identity  =  98%     Matches             =  1318   Mismatches    =  13
Gaps              =  5       Conservative Substitutions  =  0

          X    10        20        30        40        50        60        70
         GAATTCGAAACGATGGCGTCGTCGTCTGCTGTCTACCTTCACTGATGAATCATCAAGAACATCATCAATACCTCCATCCTG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CTCGAGCCATGGCGTCGTCGTCTGCTGTCTACCTTCACTGATGAATCATCAAGAACATCATCAATACCTCCATCCTG
          X    10        20        30        40        50        60        70

              80        90        100       110       120       130       140
         AACCTGCGCTACGAATCCAATCACCTGACCTGTCTCCGCTACGCTTCCAAAATCAACATCGGTTCTAAA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         AACCTGCGCTACGAATCCAATCACCTGACCTGTCTCCGCTACGCTTCCAAAATCAACATCGGTTCTAAA
              80        90        100       110       120       130       140

              150       160       170       180       190       200       210
         GTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATC
              150       160       170       180       190       200       210

              220       230       240       250       260       270       280
         CTGAAGAATGCTATCGTATACAAACTTCTCCACCTCCTTCGATCCTGATCCGTATCCCGAAA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CTGAAGAATGCTATCGTATACAAACTTCTCCACCTCCTTCGATCCTGATCCGTATCCCGAAA
              220       230       240       250       260       270       280

              290       300       310       320       330       340       350
         TACTTCAACTCCATCTCTGAACAATGAATACACCATCAACTCAACTGCATGGAAAACAATTCTGGTTGGAAA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TACTTCAACTCCATCTCTGAACAATGAATACACCATCAACTCAACTGCATGGAAAACAATTCTGGTTGGAAA
         290       300       310       320       330       340       350

              370       380       390       400       410       420       430
         GTATCCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGGTGTGTGATTC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GTATCCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGGTGTGTGATTC
         360       370       380       390       400       410       420       430

              440       450       460       470       480       490       500
         AAATACTCTCAGATGATCAACATCTCTGACTACACAATGCTGATCTTCGTTACCATCACCAACAACATCGT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         AAATACTCTCAGATGATCAACATCTCTGACTACACAATGCTGATCTTCGTTACCATCACCAACAACATCGT
              440       450       460       470       480       490       500

              510       520       530       540       550       560       570
         CTGAATAACTCCAAAATCTACATCAACGGCGCGTCTGATCGACCAGAAAACCGATCTCCAATCTGGTAACATC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CTGAATAACTCCAAAATCTACATCAACGGCGCGTCTGATCGACCAGAAAACCGATCTCCAATCTGGGTAACATC
         510       520       530       540       550       560       570

              580       590       600       610       620       630       640
         CACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGGCTACATCTGGATCAAAATAC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGGCTACATCTGGATCAAAATAC
              580       590       600       610       620       630       640

              650       660       670       680       690       700       710       720
         TTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGAACCTGTACGACAACCAGTCCAATTCTGGT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         650       660       670       680       690       700       710       720
```

```
2. US-09-910-186A-1 (1-1332)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    = 1311    Optimized Score = 1314    Significance = 0.58
Residue Identity = 98%     Matches         = 1318    Mismatches   = 13
Gaps             = 5       Conservative Substitutions = 0
```

3. US-09-910-186A-1 (1-1332)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score =	538	Optimized Score =	704
Matches =	55%	Matches =	759
Residue Identity =	71	Conservative Substitutions	

Significance = -1.15
Mismatches = 530
Gaps = 0

```
TCTGGTATCGTATTCGGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTAAACGC
   1190      1200      1210      1220      1230      1240      1250

   1250      1260      1270      1280      1290      1300      1310      1320
GAACGTTCCTCTCCGCACTCTGGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCG
   ||| | | - | - | - | |||||||| |||| |||||||||| || - || |||||| |||
AAACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGACCGAATAGTAA
   1260      1270      1280      1290      1300      1310      1320

         1330 X
CTGTAAGAATTC
   | - ||| - |
CCTCTAGAGTCGAGGCCTGCAG
   1330      1340      1350
```

```
> O <
O| |O    IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-1-inv.res made by bobryen on Thu 7 Nov 102 14:39:50-PST.

Query sequence being compared:US-09-910-186A-1' (1-1332)
Number of sequences searched:                3
Number of scores above cutoff:               3

       Results of the initial comparison of US-09-910-186A-1' (1-1332) with:
              File :US08123975A.seq
```

complement

```
100-
     -
N    -
U 50-|
M    -
B    -
E    -
R 10-|
     -
O    -
F    -
     -
S  5-|
E    -
Q    -                          *
U    -
E    -
N    -
C    -
E    -                                                                    *
S  0-|-------------------------------------------------------------------|--|--
SCORE 0    |   |   |   |   |   |   |   |   |   |   |   |   |
           6  12  18  24  31  37  43  49  55
STDEV -6  -5  -4  -3  -2  -1   0   1

                    PARAMETERS

Similarity matrix    Unitary
Mismatch penalty            1
Gap penalty              5.00         K-tuple            4
Gap size penalty         0.33         Joining penalty   30
Cutoff score                1         Window size      500
Randomization group         0

                 SEARCH STATISTICS

                 Mean      Median        Standard Deviation
Scores:           47         45                 6.35

                 CPU                    Total Elapsed
Times:       00:00:00.00             00:00:00.00

Number of residues:             4027
Number of sequences searched:      3
Number of scores above cutoff:     3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                            Init. Opt.
Sequence Name    Description                    Length Score Score  Sig.  Frame
------------     -----------                    ------ ----- -----  ----  -----
                 **** 1 standard deviation above mean ****
 1. US-08-123-975A-6 Sequence 6, Application U  1351    55   432   1.26     0
                 **** 0 standard deviation from mean ****
 2. US-08-123-975A-4 Sequence 4, Application U  1338    44   479  -0.47     0
 3. US-08-123-975A-1 Sequence 1, Application U  1338    44   479  -0.47     0
```

```
1. US-09-910-186A-1' (1-1332)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    55   Optimized Score      =   432   Significance =  1.26
Residue Identity =   40%   Matches              =   515   Mismatches   =   658
Gaps             =          87   Conservative Substitutions =        0
```

```
     80         90        100        110        120        130        140        150
CGTTCGGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAAACCGATG
                       ||   ||||  |||  |||  |||||||||||
                   ATGGCTTTCAACAAATCAATTCCGAAATCCTGAACAATATCATCCTGAACC
                   X          10        20        30        40        50

       160        170        180        190        200        210        220
AAACCGATATCGTTACCATTGTGTCCTGCAGATTCATTTTGCATTGTTGTTAGTGATACCCTGGTCGTTCTTG
                |   |  ||| |  ||    |  ||||  | |||||    |||||||
TGCGGTACAAAGACAACAATCTGATCGATCTGTCTGGTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
      50        70        80        90       100       110       120

     230        240        250        260        270        280        290
GATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGACAAGATCTTTTCTACA
||  ||||||||  |||  | |||  ||||||||    |||| |||   |||||||||||||| |||||
AACTGAATGACAAGAACCAG-TTCAAACTGACCTCTTCCGCTAACTC---------TAAGATCCGTGTTAC-
    130       140       150       160       170              180

     300        310        320        330        340        350        360
CCAGCCTGAGAAGCATTGGTAGCCCAGACACGGTATTCTTTGTTCTTAACTACAACATTGATGTATACACGATCA
|||  |||| ||| ||     |  ||||  ||||||| |  |  ||||||        |||||||||||||||
TCAGAATCAGAA--CATCATCTTCAACTCCGTATCCTGG--------------ACTTCTCTGTTCCTTCTGGATCC
    190       200       210       220                       230       240

     370        380        390        400        410        420        430
TTGTTCGAACGATATTGTCCTTGTTA-CCAGACGCGTATTCTTGATGATGAATTGGTACCACGGTACAG
||   ||||| |||||||   ||||   |||  ||| ||||  ||  |  ||||   || ||||||||||
GTATCCGAAATACAAGAACGACGGTATCCAGAATTACACTCCACAATGAATCACCATCCATCAACTGCATGA
    250       260       270       280       290       300       310

     440        450        460        470        480        490        500
GGAAGAGTTCAGGT----AGATGTTGGT-AGTCATAACAGAGACCAGCGGACCTTCAGGTACATGTAACCG
||| | |||  ||||     || |||||  ||| ||| | |||| || ||||||||   | | ||||||||
AGAATAACCTGGTTGGAAGACATCCATCCGCGGTAACCGTATCATCTGGAC---TCTGATCGATATCAACG
    330       340       350       360       370       380

     510        520        530        540        550        560        570
CGGATCACCTACATTGTTGACGTCAACGTATTTGTTCGGATCGTACAGATTCAGCATGTAGCATGACGGTTTGTCG
|||  ||||||| |||| | |||||| ||||| |||  ||   ||||| ||||||||| |||    ||||  |||
GTAAGACCAAATCTGTATTCTTCGA-ATACAACATCCGTGAAGACA---TCTCTGAATACATCAATCGCTGG
    390       400       410       420       430       440       450

     580        590        600        610        620        630        640
TACTGCAGGTAGTCACCCCAGAAGTCTTTCAGGATACCAGAAGTTGGACTGGTGTCGTACAGGTCTTTGATT
||   ||||   ||| || ||| ||  | || |||   |||||    |||  ||  |  ||||||||||||
TTCTTC--GTTACCATCACCCAATAACCTGAACATGCTAAAATCTACATCAACGGTAAACTGGAAATCTAATA
    460       470       480       490       500       510       520

     650        660        670        680        690        700        710
TCTTTTCGTTCAGTC------TTTGTCGAACAGATTGAA---GTATTTGATCCAGATTGAGCGGTGAGTG
||||||||| |||||       | | ||||| | ||| ||     | ||  || ||||   ||||| |||
CCGACATCAAAGACATCCGTGAATTATCCGGTAACATGCTAACTGACGGTGACATCGGTGACATCGATC
    530       540       550       560       570       580       590

     720        730        740        750        760        770
TCAACGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAG-----ATTGGAGATC
```

2. US-09-910-186A-1' (1-1332)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score   = 44   Optimized Score = 479   Significance = -0.47
Residue Identity = 43%   Matches   = 584   Mismatches   = 689
Gaps   = 85   Conservative Substitutions = 0

3. US-09-910-186A-1' (1-1332)
US-08-123-975A-1 Sequence 1, Application US/08123975A

```
Initial Score     =     44    Optimized Score   =    479    Significance  =  -0.47
Residue Identity  =    43%    Matches           =    584    Mismatches    =    689
Gaps              =     85    Conservative Substitutions =     0
```

```
      1200      1210      1220      1230      1240      1250
AACCGATGTTGATTT--TGGAAGCGTAGCGAGACAGGTCGATCAGGTGATTGGATTCGTAGCGCAGGT----
|||||| ||||||||  ||||||||||||||||||| || ||  || ||||||||||| |  | |||
TAACGATATCGGTTCATCGGTTCCACCAGTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAA
1170      1180      1190      1200      1210      1220      1230

1260      1270      1280      1290      1300      1310      1320
---TCAGGATGGAGGTATTGATGATGTTC----TTGATGTATTCAGTGAAGTAGACAGCAGACGGCATCGTT
|||| |||||||| ||  |||| |||||    ||| |||||||||| |   |||| |  ||||| | |
TCGTCAGATCGAACGTTCCTCGCACTCTGGGTTGCTCTGGAGTTCATCCCGGTTGATGACGGTTGGGG
1240      1250      1260      1270      1280      1290      1300

    1330 X
TCGAATTC
| | | ||
TGAACGTCCGCTGTAACCCGGGAAAGCT
1310      1320      1330
```

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> O <
O| |O   Intelligenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-2.res made by bobryen on Thu 7 Nov 102 14:31:34-PST.

Query sequence being compared:US-09-910-186A-2 (1-437)
Number of sequences searched:                3
Number of scores above cutoff:               3

Results of the initial comparison of US-09-910-186A-2 (1-437) with:
         File : US08123975A.pep
```

```
Sequence Name      Description                                        Length  Init. Opt.   Sig. Frame
                                                                              Score Score
------------------------------------------------------------------------------------------------------
                                **** 1 standard deviation above mean ****
  1. US-08-123-975A-3  Sequence 3, Application U                        415   415   415    1.16    0
                                **** 0 standard deviation from mean ****
  2. US-08-123-975A-5  Sequence 5, Application U                        439   273   193   -0.52    0
  3. US-08-123-975A-2  Sequence 2, Application U                        850   276   180   -0.62    0


  1. US-09-910-186A-2 (1-437)
     US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =   415    Optimized Score       =   415    Significance   =   1.16
Residue Identity =   100%   Matches               =   415    Mismatches     =     0
Gaps             =     0    Conservative Substitutions =    0


              10        20 X      30        40        50        60        70
     LLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                          RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                        X           10        20        30        40        50

             80        90       100       110       120       130       140
     YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI
     YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI
             60        70        80        90       100       110       120

            150       160       170       180       190       200       210
     NISDYINRWIFVITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
     NISDYINRWIFVITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
            130       140       150       160       170       180       190

            220       230       240       250       260       270       280       290
     ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYDVNNVGIRGYMYLKGPRGSVMTTNIY
     ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYDVNNVGIRGYMYLKGPRGSVMTTNIY
            200       210       220       230       240       250       260

            300       310       320       330       340       350       360
     LNSSLYRGTKFIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
     LNSSLYRGTKFIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
            270       280       290       300       310       320       330       340

            370       380       390       400       410       420       430
     VMKSKNDQGTNRCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGE
     VMKSKNDQGTNRCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGE
            350       360       370       380       390       400       410

     X
     RPL
     |||
     RPL
     X


  2. US-09-910-186A-2 (1-437)
     US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =   193    Optimized Score       =   273    Significance   =  -0.52
Residue Identity =    38%   Matches               =   169    Mismatches     =   230
Gaps             =    17    Conservative Substitutions =    26


            X     10        20        30        40        50        60        70
     MRLLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNA
          |  || || | |:: |  | |||||   ||:|:|   ||  |||| ::|| | :: |  ||  |  |||
     FNKYNSEILNNILNLRYKDNNLIDLSGYGAKVEVYDGVELN--DKNQFKLTSSANSKIRVTQNQN
            X     10        20        30        40        50        60
```

```
                                                                          *
      |    |    |    |    |    |    |    |    |  * *    |    |    |
   0  |    |    |    |    |    |    |    |    |         |    |    *  |
100-
  - N
  - U
 50- M
  - B
  - E
  - R
  -
  - O
 10- F
  -
  - S
  5- E
  - Q
  - U
  - E
  - N
  - C
  - E
  0- S

SCORE 0   46  92  138  184  231  277  323  369  415
STDEV    -1                 0              1

                   PARAMETERS

Similarity matrix    PAM-150    K-tuple              1
Threshold level of sim.  16%    Joining penalty     20
Mismatch penalty       1        Window size        437
Gap penalty          5.00
Gap size penalty     0.05
Cutoff score         1
Randomization group  0

                   SEARCH STATISTICS

Scores:    Mean     Median     Standard Deviation
           262      181        132.08

              CPU                Total Elapsed
Times:   00:00:00.00            00:00:00.00

Number of residues:            1704
Number of sequences searched:     3
Number of scores above cutoff:    3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                680        690        700        710        720        730        740
ASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGI-TNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVA----
340        350        360        370        380        390        400
                        :   |  :|:    ||||      ::    :     :   :|:|
KYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDESTDEIGLIGIHRFYESGIVFEEYKD
750        760        770        780        790        800        810

                                    X
---SNWYNRQIERS--SRTLGCSWEFIPVDDGWGERPL
410        420        430
|-|:|:     |||||| | ||:||:|
YFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
820        830        840        850
```

3. US-09-910-186A-2 (1-437)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

```
Initial Score       =    180   Optimized Score  =    276   Significance = -0.62
Residue Identity =    37%   Matches          =    170   Mismatches   =    235
Gaps             =    17    Conservative Substitutions       =     26
```

```
                        X           10        20        30        40        50
                MRLLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDK
                        |   :| ||:| |  :::::  ::      :      ||
KVNKYLKTIMPFDLSIYNDTLIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEYDGVELN--DK
390        400      X 410        420        430        440        450

        60        70        80        90       100       110       120
NQIQLFNLESSKIEVILKNAIVVNSMYENFSTSFWIRIPKYFNSIS--LNNEYTIINCMENNSGWKVSLNY
|   || :||     |  :|: || ||||||||||||||||||||   ||||||||||||||||||:
NQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRG
460        470        480        490        500        510        520

       130       140       150       160       170       180       190
GEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIIDQKPISNLGNIHASNN
|||| |  |  :|   :|:||||||    ||||||||||||||   |||||:|||||||||:|||   ::
NRIIWTLIDINGKTKSVFFEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE
530        540        550        560        570        580        590

       200       210       220       230       240       250       260
IMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVD
|| | ||  |||| |||||: |  |  : |  ||:::| | | |    | |||| ||||||||||||||||:
IIFKLDGDIDRTQFIWMKYFSFINTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIK
600        610        620        630        640        650        660        670

       270       280       290       300       310       320       330
VNNVGIRGYMYLKGPRGSVMTNIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATN
 | | ||||||||||| |  ||||||||:|:|||||||||:|| :|| |||||:|||||||:|||||:|:
LKKDSPVGEILTRSKYNQNSKIYNYRDLYIIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFNLNQEWRVTY
```

```
        80        90       100       110       120       130       140
IVINSMYENFSTSFWIRIPKYFNSIS---LNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFK
|::||:   || ||||||||||||||   ||||||||||||||||||||:||||||| |  |  :|   :|
IIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFE
70        80        90       100       110       120       130

       150       160       170       180       190       200       210
YSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYF
|   ||||||||||||||||   |||||:|||||||||:|||   ::   || | ||  ||||
YINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYF
140        150        160        170        180        190        200

       220       230       240       250       260       270       280
NLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVM
  |  : |  ||:::| | | |    | |||| |||||||||||||||||:  | | ||||||||||| |
SIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNS
210        220        230        240        250        260        270

       290       300       310       320       330       340       350
TTNIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGN
||||||||:|:||||||||||:|| :|| |||||:|||||||:|||||:|:      :   |  :|
KYINYRDLYIIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFNLNQEWRVTYKYFKKEEEKLFLAPISDSDE
280        290        300        310        320        330        340        350

       360       370       380       390       400       410
LSQVVVMKSKNDQGI-TNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVA------SNWYNRQIERS--SRT
|   :     :   :|:|            ::    :     :   :|:|     |-|:|:
FYNTIQIKEYDEQPTYSCQLLFKKDESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLK
360        370        380        390        400        410        420

       420         X 430
LGCSWEFIPVDDGWGERPL
||| | || | ||:||:|
LGCNWQFIPKDEGWTE
430        X
```

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-3.res made by bobryen on Thu 7 Nov 102 14:40:15-PST.

Query sequence being compared:US-09-910-186A-3 (1-1323)
Number of sequences searched:          3
Number of scores above cutoff:         3

Results of the initial comparison of US-09-910-186A-3 (1-1323) with:
       File :US08123975A.seq
```

```
Sequence Name       Description                                              Length  Init.   Opt.   Sig. Frame
                                                                                     Score   Score
---------------------------------------------------------------------------------------------------------------
1. US-08-123-975A-4  Sequence 4, Application U                               1338    1304    1305    0.58   0
2. US-08-123-975A-1  Sequence 1, Application U                               1338    1304    1305    0.58   0
                     **** 1 standard deviation below mean ****
3. US-08-123-975A-6  Sequence 6, Application U                               1351     538     704   -1.15   0
```

```
1. US-09-910-186A-3 (1-1323)
   US-08-123-975A-4  Sequence 4, Application US/08123975A

   Initial Score    =   1304    Optimized Score =   1305    Significance   =   0.58
   Residue Identity =   98%     Matches         =   1309    Mismatches     =   14
   Gaps             =            Conservative Substitutions =   5            =   0
```

```
                  x          10         20         30         40         50         60
    GAATTCGAAACGACGATGCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCAATCCTGA
                                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CTCGAGCCATGGCTCGTCTGCTGTCTCACCTTCACTGAATACATCAAGAACATCATCAATACCTCCAATCCTGA
         10         20         30         40         50         60         70

                  70         80         90         100        110        120        130
    ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGGTTCCAAAATCAACATCGGTTCTAAAG
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGGTTCCAAAATCAACATCGGTTCTAAAG
         80         90         100        110        120        130        140

                  140        150        160        170        180        190        200
    TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGAATCTTCCAAAATCGAAGTTATCC
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGAATCTTCCAAAATCGAAGTTATCC
         150        160        170        180        190        200        210

                  210        220        230        240        250        260        270        280
    TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
         220        230        240        250        260        270        280

                  290        300        310        320        330        340        350
    ACTTCAACTCCATCTCTCTGAACAATGAATACAACTGCATGATGAAAACAATTCGGTTGGAAAG
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ACTTCAACTCCATCTCTCTGAACAATGAATACAACTGCATGATGAAAACAATTCGGTTGGAAAG
         290        300        310        320        330        340        350

                  360        370        380        390        400        410        420
    TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACGACTCAGGAAATCAAACAGCGTGTTGTATTCA
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACGACTCAGGAAATCAAACAGCGTGTTGTATTCA
         370        380        390        400        410        420        430

                  430        440        450        460        470        480        490
    AATACTCTCAGATGATCAACAATCCTGACTACATGCTGGATCTTCGTTACCATCACCAACAATCGTC
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AATACTCTCAGATGATCAACAATCCTGACTACATGCTGGATCTTCGTTACCATCACCAACAATCGTC
         440        450        460        470        480        490        500

                  500        510        520        530        540        550        560
    TGAATAACTCCAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TGAATAACTCCAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
         510        520        530        540        550        560        570

                  570        580        590        600        610        620        630        640
    ACGGCTTCTAATAACATCATGTTCAAACTGGACGCGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ACGGCTTCTAATAACATCATGTTCAAACTGGACGCGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
         580        590        600        610        620        630        640

                  650        660        670        680        690        700        710
    TCAATCTGTTCGACAAGAGACTGAACGAAAAAGAAATCAAAGACCTGTACGAACCAGTCCAATTCTGGTA
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
SCORE  0    |    |    |    |    |    |    |    |    |    |
      145   290  435  580  724  869  1014 1159 1304
STDEV  -1

100- |
     N
  50- U
     M
     B
     E
     R
     O        *
  10- F
     S
   5- E
     Q
     U
     E
     N         *
     C
   0- E ------------------------------------------------
     S
```

```
                PARAMETERS

Similarity matrix   Unitary   K-tuple              4
Mismatch penalty    1         Joining penalty      30
Gap penalty         5.00      Window size          500
Gap size penalty    0.33
Cutoff score        0
Randomization group

                SEARCH STATISTICS

Scores:    Mean    Median      Standard Deviation
           1048    539         442.25

Times:     CPU                 Total Elapsed
           00:00:00.00         00:00:00.00

Number of residues:              4027
Number of sequences searched:    3
Number of scores above cutoff:   3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACCTGCGCTACGGATCCAATCACCTGACCTGTCTCGCTACGGTTCAACATCAGGTTCTAAAG
      80        90       100       110       120       130      140

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TTAACTTCGATCCGATCGACAAGAATCAGATCGTGTTCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
     140       150       160       170       180       190       200      210

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGAAGAATGCTATCGTATCAACTCTATGTACGAAAAACTTCTCCACCTCCTTCTGGATCCGTATCCGAAAT
     210       220       230       240       250       260       270      280

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACTTCAACTCCATCTCTGAACAATGAATACACCATCAACAACTGCATGGAAAACAATCTGGTTGGAAAG
     290       300       310       320       330       340      350

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TATCTCTGAACTACGGTGAAATCATCTGGACTCTGGAGGACCACTCAGGAAATCAAACAGCGTGTTGTATTCA
     360       370       380       390       400       410      420

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AATACTCTCAGATGATCAACATCTCTGACTACTACATCGCTTACCATCACCATCAACCAACAATCGTC
     430       440       450       460       470       480      490

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGAATAACTCCAAAATCTACATCTACACGGCCGTGTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
     500       510       520       530       540       550      560

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACGGTTCTAATAACATGTTCAAACTGGACGGTGCGTCGCGTACCACTGGATCCGGTGAGATCGGATCAAAATACT
     570       580       590       600       610       620      630      640

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCAATCTGTTCGACAAAGAACTGAACCAGAAAGAAAGAAAATCAAAGACCGTACGACAAACCGTCCAATTCTGGTA
     650       660       670       680       690       700      710      720

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCCTGAAAGACTTCTGGGGTGAACGGTCCCGTTCAAACAATATCCGGTTATACCTGAATCGTTACGGATCCGA
     720       730       740       750       760       770      780      790

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACAAATACGTTGACGTCAACAATGTCAAATGTAGGTATCCCGGTTACATGTACCTGAAAGGTCCGGCGGTCTG
     790       800       810       820       830       840      850

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGACTACCAACAACATCTTCCCTGGTACCGTTTCCCTGTACCTGGTTACCTGAAAATCATCAAGAAATACGCGGTCTG
     860       870       880       890       900       910      920      930

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GTAACAAGGACCAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTGAAGAACAAAGAATACC
     930       940       950       960       970       980      990     1000
```

```
TCAATCTGTTCGACAAAGAACTGAACCAGAAAGAAAGAAAATCAAAGACCTGTACGACAAACCGTCCAATTCTGGTA
650       660       670       680       690       700       710      720

TCCTGAAAGACTTCTGGGGTGAACGGTCCCGTTCAAACAATATCCGGTTATACCTGAATCGTTACGATCCGA
720       730       740       750       760       770       780      790

ACAAATACGTTGACGTCAACAATGTCAAATGTGTAGGTATCCCGGTTACATGTACCTGAAAGGTCCGGCGGTCTG
790       800       810       820       830       840       850

TGACTACCAACAACATCTTCCCTGGTACCGTTTCCCTGTACCTGGTTACCTGAAAATCATCAAGAAATACGCGGTCTG
860       870       880       890       900       910      920       930

GTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTGAAGAACAAAGAATACC
930       940       950       960       970       980       990      1000

GTCTGGCTACCAATGGTTCTCAGGCGTTGTGTGTAGAAAAGACTTGTCTGCTCTGGAAATCCCGGACGTTGGTA
1010      1020      1030      1040      1050      1060      1070

ATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGGACCAGGGTATCGACTAACACTAACAATGAATCTGC
1080      1090      1100      1110      1120      1130      1140      1150

AGGACAACAATGGTTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAAACAATATCGGCTAAACTGGTTGCTT
1150      1160      1170      1180      1190      1200      1210      1220

CCAACTGGTACAACGTCAGATCGAAGTCGTCCTCTCGCACTGTCGGGTTGCTTGGGAGTTCATCCCGGTTG
1220      1230      1240      1250      1260      1270      1280      1290

ATGACGGTTGGGGTGAACGTCCCGCCTGTAA----GAATTC    X
1290      1300      1310      1320              X
```

2. US-09-910-186A-3 (1-1323)
US-08-123-975A-1 Sequence 1, Application US/08123975A

```
Initial Score     =  1305   Significance  =  0.58
Optimized Score   =  1304   Mismatches    =    14
Matches           =  1309   Gaps          =     0
Residue Identity  =   98%
Conservative Substitutions  =  5
```

```
              X
          10        20        30        40        50        60        70
GAATTCGAACGACGTCTCGCTCTGACCTTCACTGAATACATACAAGAGAACATCAATACCTCCATCCTGA
     10        20        30        40        50        60        70
CTCGAGCCGATGGCTCGTTCGCTGCTTCACCTGACCTGTCTCGCTACGGTTCAACATCAGGTTCTAAAG
     70        80        90       100       110       120       130
```

```
3.  US-09-910-186A-3 (1-1323)
    US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score   = 538    Optimized Score = 704    Significance = -1.15
Residue Identity = 55%   Matches         = 763    Mismatches   = 526
Gaps            = 74     Conservative Substitutions = 0
```

```
TATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAGTTAAACGCAAACC
    1200      1210      1220      1230      1240      1250      1260

    1250      1260      1270      1280      1290      1300      1310
TTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTA
 |-| |||||||||| |||| |||||||||||| ||-|| ||||| |||- |
GTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTCT
    1270      1280      1290      1300      1310      1320      1330

1320 X
AGAATTC
||||
AGAGTCGAGGCCTGCAG
    1340      1350
```

```
> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-3-inv.res made by bobryen on Thu 7 Nov 102 14:40:46-PST.

Query sequence being compared:US-09-910-186A-3' (1-1323)
Number of sequences searched:                3
Number of scores above cutoff:               3

   Results of the initial comparison of:US-09-910-186A-3' (1-1323) with:   [complement]
       File : US08123975A.seq
```

```
100-
    -
N   -
U 50-
M   -
B   -
E   -
R   -
    -
O   -
F 10-
    -
S 5-
E   -
Q   -
U   -
E   -                              *
N   -                                              *
C   -                                           ---|--
E 0-------------------------------------------|----|----
S         |----|----|----|----|----|----|----|----|--|--55
SCORE 0    16   12   18   24   31   37   43   49    1
STDEV -6   -6   -5   -4   -3   -2   -1    0
```

```
                    PARAMETERS

Similarity matrix    Unitary
Mismatch penalty     1
Gap penalty          5.00          K-tuple          4
Gap size penalty     0.33          Joining penalty  30
Cutoff score         1             Window size      500
Randomization group  0
```

```
              SEARCH STATISTICS

                Mean    Median    Standard Deviation
Scores:          47       45           6.35

                 CPU            Total Elapsed
Times:        00:00:00.00       00:00:00.00

Number of residues:            4027
Number of sequences searched:     3
Number of scores above cutoff:    3
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
                                                      Init.  Opt.
Sequence Name    Description                   Length Score  Score  Sig.  Frame
---------------  --------------------------    ------ -----  -----  ----  -----
                            ****  1 standard deviation above mean  ****
 1. US-08-123-975A-6  Sequence 6, Application U  1351   55    429   1.26    0
                            ****  0 standard deviation from mean  ****
 2. US-08-123-975A-4  Sequence 4, Application U  1338   44    475  -0.47    0
 3. US-08-123-975A-1  Sequence 1, Application U  1338   44    475  -0.47    0
```

```
 1. US-09-910-186A-3' (1-1323)
    US-08-123-975A-6  Sequence 6, Application US/08123975A

Initial Score    =   55      Optimized Score      =  429    Significance = 1.26
Residue Identity =   40%     Matches              =  518    Mismatches   =  663
Gaps             =           89      Conservative Substitutions =         0
```

```
          80        90       100       110       120       130       140       150
CGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAAACCGATG
                        ATGGCTTTCAACAAATACAACATTCCGAAATCCTGAACAATATCATCCTGAACC
                        x         10        20        30        40        50

         160       170       180       190       200       210       220
AAACCGATATCGTTACCATTGTGTCCTGCAGATTCATTTGCATTTGTTAGTGATACCCTGGTCGTTCTTG
           |||       |||   |||       ||||  ||  |||       ||  |||  ||||||
TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
            60        70        80        90       100       110       120

         230       240       250       260       270       280       290
GATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGCAAGAGATCTTTTCTACA
    |||       |||||  ||||      |||     |||||||||||||||       |||||||||||
AACTGAATGACAAGAACCAG-TTCAAACTGACCTCTCCGCTAACTC--------TAAGATCCGTGTTAC-
     130       140       150       160       170                180

         300       310       320       330       340       350       360
CCAGCCTGAGAAGCATTGGTAGCCAGACGGTATTCTTGTTCTTAACTACAACATTGATGTATACACGATCA
      |||||  |||    ||||  |||||||| |||||||||||||       |||||||||||||||
TCAGAATCAGAA-CATCACTTCAACTCCGTATTCCTG------------ACTTCTCGTTCCTTCGGATCC
     190       200       210       220                230       240

         370       380       390       400       410       420       430
TTGTTGCGAACGATATTGTCCTTGTTA-CCAGACGCGTATTCTTGATGATGAATTGGTACCACGTACAG
  |||||  ||||||  |||||       ||||||   |||     ||||||||  |||||||||||||
GTATCCCGAAATACAAGAACGACGACGGTATCCGAAGAATTGGACTGGTTGTCGTGTACACAGTCTTGA
     250       260       270       280       290       300       310

         440       450       460       470       480       490       500
GGAAGAGTTCAGGT----AGATGTTGGT-AGTCATAACAGAACCACGGGGACCTTTCAGGTACATGTAACCG
||| ||| ||||| |    |||  ||    ||| |||||||||||||||||||   |||||||||||||||
AGAATAACTCGGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCGTGGAC---TCTGATCGATATCAACG
     320       330       340       350       360               370       380

         510       520       530       540       550       560       570
CGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGATCGTACAGATTCAGCATGTAGTACGGTTTGTCG
  ||  |||  |||| |||    ||      ||||||||||||||    ||||| ||||||||||||||||
GTAAGACCAAAATCTGTATTCTTCGA-ATACAACATCCGTGAAGACA---TCTCTGAATACATCACTGCTGG
     390       400       410       420       430               440       450

         580       590       600       610       620       630       640
TACTGCAGGTAGTCACCCCAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCGTGTACACAGGTCTTTGATT
| ||| ||||     ||  ||    ||||||||||||||   |||||||||||||||   |||||  ||||||
TTCTTC--GTTACCATCACCAATAACCTGAACATGTCTAAAATCACAACTTCAACTGGAAATCTAATA
     460       470       480       490       500               510       520

         650       660       670       680       690       700       710
TCTTTTCGTTCAGTTC-----TTTGTCGAACAGATTGAA---GTATTTGATCCAGATGTAGCCGGTGAGTG
  || ||||||     |    |||||      ||  |||      ||| ||  ||||||||||||||||
CCGACATCAAAGACATCCGTGAAGTTATCCTACGGTGAATCATCTGAAATCAACTGGACGGTGACATCGATC
     530       540       550       560       570               580       590

         720       730       740       750       760       770
TCACGACAACCGTCCAGTTTGAAACATGAATGTTATTAGAAGCGTGCGATGTTACCCAG-----ATTGGAGATC
```

```
                    60          70          80          90         100         110
ACCGATGAAACCGATATCGTTACCATTGTTGTCTGCAGATTCATTTGTGTTAGTGATATCCTGGTC
  ||   |||||    ||  ||   |  |||      | |   | |||  |||  ||
GGTTCCAAAATCAACATCGGTTCTAAAGTTAACTT--CGATCCGACGACGAATTCAGATGTGATGGTA
       120         130         140         150         160         170         180

                   200         210         220         230         240         250
GTTCTTGGATTCATTACAACTACCTGAGACAGATTACCAACGTCCGGATTCCAGAGACCAGACAAGATCTT
  ||||||||||||      |     ||   | | |     |||  | |||   ||
AATCTGGAATCTCCAAAATCGAAGTATCC---TGAAGAATGCTATCGTATACAACTCTATGTACGAAAC
       190         200         210         220         230         240         250

          300         310         320         330         340         350         360
TTCTACACCAGCTGAGAAGCATTGGTAGCACGGTATTCTTTGTTCTTAATACAACATTGATGATATAC
      |||    |  ||     |||| |   ||   || ||   | || |  |   |   |  |||||
TTCTTCCACCTCCTT---CTGGATCCGTATCC---CGAAATACTTCAACTCTCTGAACAATGAATAC
       260         270         280         290         300         310         320

                  380         390         400         410         420
ACGATCAT---TGTTCCGACGATATTGTCCTTGTTACCAGACGC-GTATTTCTTGATGATGAATTTGGTA
  | |  ||    ||  |||     |      |||    | ||  |   |   | ||  |   ||| |||
ACCATCATCAACTGCATCGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTCTGAACATCTGGACT
       330         340         350         360         370         380         390

       440         450         460         470         480         490
CCACGGTACAGGGAAGAGTTCAGGTAGAGTTGGTAGTC--ATAACAGAACCACGCGGACCTTTCAG-GTAC
  | | |   |||     ||   |||      |   ||      |  ||    ||    |   |   |||
CTGCAGGACACTCAGGAATCAAACAGCGTGTTGTATTCAAATCTGAATAACTCTACATCAACG
       400         410         420         430         440         450         460

                  510         520         530         540         550         560
ATGTAACCGCGGATACCTACCATTGTTGACGTCACC---CCAGAAGTCTTTCAGGATACCAGATTGGACTGGTTCG
  | |      |    | |   | |  |  ||  | ||     ||     |    |||   |  |  |   |  | ||
ATCAATCGGTCGGAT-----CTTCGTTACCAACATCCAATCGGTCAATAACTCTAATAACTCTACATCAACG
       470         480         490         500         510         520         530

       580         590         600         610         620         630
ACGGTTTG-TCGTACTGCAGGTAGTCACC---CCAGAAGTCTTTCAGGATACCAGATTGGACTGGTTGTCGG
   |  |    | | |     | | |  |       ||     ||| ||     |   |  |  |  |   | ||
GCCGTCTCGATCGGACGAAACCGATCTCCAATCGGTAA---CTTAATAACTCTAATAACTCTACAACG
       540         550         560         570         580         590         600

          650         660         670         680         690         700
TACAGGTCTTGATTCTTTTTCGTTCAGTTCAGTCTTGTGTCGAACAGAGTTGATCCAGATTGATGATGGG
   | || | | |||     | ||    |   | | || ||   |     | | | |   |   | | |
TGGACGGTTGTCGTGACACTGAGATTCAAATCTGGATCCGTACACGGTGGATATTGATTCGTCGACAAGAGAACG
       610         620         630         640         650         660         670

       720         730         740         750         760         770
TGAGGTCACGACACCGTCCAGTTGAACATGATGTATTAGAAGGTGGATGTTACCCAGATTGGAGATC
   ||  |    |   |  |  |   |   |  |  ||  |   |    | | |    |   ||  |
AAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCGGTATCTCGGTAATCTGAAAGACTTCTGG---GGTGACT
       680         690         700         710         720         730         740

          790         800         810         820         830         840         850
GGTTTCTGGTCGATCAGACGCCGTTGATGTAGAGTTTGGAGTTATTCAGAGTCGATGTTGACGTAACG
   || | | || | |  |    |    | |  |  | ||   | || |  |  |  | ||||||
ACCTGCAGTACGA-CAAACCGTACTACATCAACCGTA--CGATCCGAACAAATACGTTGACGTCAACA
       750         760         770         780         790         800         810

AAG-----ATCCAGCGGATTGAGTCAGTGAGTCAGATGTTGATCATCGTGGTATTGAATACAACACGCTGTT
         ||  ||     |  |   |   |  ||||  ||  | |   | |   |  |  |    |
ATGTAGGTATCCGCGGTTACATGTA--CCTGAAAGGTCCGGTTCTGT-TATGACTACCAACATCACC
       820         830         840         850         860         870         880

          930         940         950         960         970         980
TGATTTCCTGAGTGTCCTGCAGAGTCCAGATGATTCACCGTAGCTTCAGGCGATATTGTTGAACTGGTGGAA
   |  |  |||   |   || ||  |||  |   || |   |  |   |    |   |
AGAGGAACGTTCGATCTGACGATTGTACCAGTTAGCCGATATTGTTGAACTTTCCAACCGAATATC
       890         900         910         920         930         940         950
```

2. US-09-910-186A-3' (1-1323)
US-08-123-975A-4 Sequence 4, Application US/08123975A

```
Initial Score    =    44    Optimized Score    =    475    Significance    =    -0.47
Residue Identity =    43%    Matches            =    583    Mismatches      =    677
Gaps             =    82    Conservative Substitutions =   0
```

```
                  10          20          30          40          50          60          70
GAATTCTTACAGGCGACGTTCACCCGACCGTCATCAACCGGTGCAACTCCCAAGAGCAACTCCCAGAGACGTCG
  ||| |||      |     ||  | ||||   |  |   || |   | |   |   | | ||   |
CTCGGAGCCCATGGCCTTCGTC-TGCTGTCTACCTGGGGATAATTGTTGTTGAACTGGTGGAA
     X           10          20          30          40          50

          80          90         100         110         120         130         140
AGAGGAACGTTCGATCTGACGATTGTACCAGTTAGCGGAGCAACCAGTTTAGCGGATATTGTTGAACTGGTGGAA
  ||| |||     || ||||   | |   |||   |  | | |   ||  |   |      |     | |
ATCAATACCTCCATCCTGA------ACCTGCGCTACGAATCAATCACCTGATCGACCTGTCTCCGCT--AC
     80          90         100         110         120         130         140
```

TGGTACCTGAAGGA
          1240

3. US-09-910-186A-3' (1-1323)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	44	Optimized Score	=	475	Significance	=	-0.47
Residue Identity	=	43%	Matches	=	677	Mismatches	=	583
Gaps	=	0	Conservative Substitutions	=	82			

[Page consists of dense nucleotide sequence alignment data displayed in rotated orientation, showing paired sequence lines with match markers (|) and base-position numbering from approximately 10 through 1320.]

```
  |  ||||| | |||||  : |    |  |    ||    ||     |||||| |  :    |  ||| ||
  TAACGATATCGGTTTCATCGGTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACA-
  1170      1180      1190      1200      1210      1220      1230

         1270      1280      1290      1300      1310      1320  x
  GATGGAGGTATTGATGATGTCTTGATGTATTCAGTGAAGT----AGACATCGTTTCGAATTC
  | | |  ||| | |  ||||| |||| | | ||  | |  |  | ||  |||  | |
  -ATCGTCAGATCGA--ACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCGGTTGATGACGGTT
  1240      1250      1260      1270      1280      1290      1300

  GGGGTGAACGTC
  1310
```

```
> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-4.res made by bobryen on Thu 7 Nov 102 14:32:06-PST.

Query sequence being compared:US-09-910-186A-4 (1-434)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

   Results of the initial comparison of US-09-910-186A-4 (1-434) with:
        File : US08123975A.pep
```

```
                                                                    Init. Opt.
Sequence Name          Description                         Length Score Score  Sig. Frame
---------------------------------------------------------------------------------------------
                      **** 1 standard deviation above mean ****
  1. US-08-123-975A-3  Sequence 3, Application US           415   416   416    1.15    0
                      **** 0 standard deviation from mean ****
  2. US-08-123-975A-5  Sequence 5, Application U             439   193   273   -0.53    0
  3. US-08-123-975A-2  Sequence 2, Application U             850   180   275   -0.63    0
```

```
1. US-09-910-186A-4 (1-434)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =  416     Optimized Score       =  416     Significance  =  1.15
Residue Identity = 100%     Matches               =  415     Mismatches    =     0
Gaps             =    0     Conservative Substitutions =   0

                 10        20        30        40        50        60        70
        MSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
              RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY
          X      10        20        30        40        50

                 80        90       100       110       120       130       140
        NSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMIN
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        NSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMIN
          60        70        80        90       100       110       120

                150       160       170       180       190       200       210
        ISDYINRWIFVTTNNRLNNSKIYINGRLLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKE
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        ISDYINRWIFVTTNNRLNNSKIYINGRLLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKE
        130       140       150       160       170       180       190

                220       230       240       250       260       270       280
        LNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVWTTNIYL
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        LNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVWTTNIYL
        200       210       220       230       240       250       260

                290       300       310       320       330       340       350       360
        NSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVV
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        NSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVV
        270       280       290       300       310       320       330       340

                370       380       390       400       410       420       430
        MKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGER
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        MKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGER
        350       360       370       380       390       400       410

        X
        PL
        ||
        PL
        X
```

```
2. US-09-910-186A-4 (1-434)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    = 193      Optimized Score       = 273      Significance  = -0.53
Residue Identity = 38%      Matches               = 169      Mismatches    =  230
Gaps             =  17      Conservative Substitutions =  26

                 10        20        30        40        50        60        70
        MSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY
                |||   |:: | || | :::: |:| || | : ::    :||   | |  :   ||| |::
              FNXYNSEILNIILNLRYKDNNLIDLSGYGAKVEVTDGVELN--DKNQFKLTSSANSKIRVTQNQNIIF
          X      10        20        30        40        50        60
```

```
100-|
    |
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   Q|
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   E|
   N|
   C|
   E|                                                              *
   S| - - - - - - - - - - - - - - - - - - - - - - - - - *   *
 0-|                                         *  *
    |_____|_____|_____|_____|_____|_____|_____|_____|
      46       92      139      185      231      277      324      370      416
SCORE 0   -1
STDEV
```

```
                PARAMETERS

Similarity matrix    PAM-150          K-tuple              1
Threshold level of sim. 16%          Joining penalty     20
Mismatch penalty        1            Window size        434
Gap penalty          5.00
Gap size penalty     0.05
Cutoff score            1
Randomization group     0

                SEARCH STATISTICS

Scores:        Mean      Median     Standard Deviation
               263        181          132.66

                CPU
Times:       00:00:00.00             Total Elapsed
                                      00:00:00.00

Number of residues:             1704
Number of sequences searched:      3
Number of scores above cutoff:     3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                            680        690        700        710        720        730        740

        340                                                                                              400
        AGVEKILSALEIPDVGNLSQVVVMKSKNDQGI-TNKCKMNLQDNGNDIGFIGFHQFNNIAKLVA-------
        ||| :  |||||  :|| |||:  || |:|:  |  ||| :||||  ||||||  ||:||||||
        KKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFBEYKDYFC
        750        760        770        780        790        800        810

                                                    X
                 410                       420
        -SNWYNRQIERS--SRTLGCSWEFIPVDDGWGERPL
        ||:||  :: ||| :|| ||| ||||||:||
        ISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
        820        830        840        850
```

```
        80          90         100        110        120        130        140
NSMYENFSTSFWIRIPKYFNSIS---LNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQ
|||  || :|||||||||||||   ||||||||||||  ||||| |:: |||||||||:|||  | |||
NSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNI
70          80          90         100        110        120        130

        150        160        170        180        190        200        210
MINISDYINRWIFVTITNRLNNSKIIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYINIKYFNLF
||::|||||| : |||:|||::|  |||||||||| :|||||:|||||||||
REDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIF
140         150         160         170         180         190         200         210

        220        230        240        250        260        270        280
DKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTN
||  |||  : | |:|| || ||| |  || |:|||||||||||||||
NTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYI
220         230         240         250         260         270         280

        290        300        310        320        330        340        350
IYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ
:  ::| :|  |  |  | ||| :| | ||: |
NYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYN
290         300         310         320         330         340         350

        360        370        380        390        400        410        420
VVVMKSKNDQGI-TNKCKMNLQDNGNDIGFIGFHQFNNIAKLVA-------SNWYNRQIERS--SRTLGC
:  |  ||: ::  ||| || : :||||| | ||||  || |  |      ||:||  ::  ||| :||
TIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFBEYKDYFCISKWYLKEVKRKPYNLKLGC
360         370         380         390         400         410         420

        430
SWEFIPVDDGWGERPL
||| ||||:||||
NWQFIPKDEGWTE
430          X
```

3. US-09-910-186A-4 (1-434)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

```
Initial Score    =    180    Optimized Score    =    275    Significance   =   -0.63
Residue Identity =    37%    Matches            =    233    Mismatches     =    233
Gaps             =    17     Conservative Substitutions     =    26
```

```
                X          10         20         30         40         50
                MSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQI
                ||:||:|:|   ||| |||||||| | :|| | :: :| ||
KYLKTIMPFDLSIITNDTILIEMENKYNSEILNNIILNLRYKDNNLLIDLSGYGAKVEVYDGVELN--DKNQF
390         400         410         420         430         440         450

        60          70          80          90         100        110        120
QLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSIS--LNNEYTIINCMENNSGWKVSLNYGEI
|||:|||||: ::|  ||:| |:||:|||||||||||||||   |||||||||||||||:|||| :
KLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRI
460         470         480         490         500         510         520         530

        130        140        150        160        170        180        190
IWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNRLNNSKIIYINGRLIDQKPISNLGNIHASNNIMF
|||| |:||| : ||:|:||  | |||||||| :||||  |:|||:|
IWTLIDINGKTKSVFFEYNIREDISEYINRWFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIF
540         550         560         570         580         590         600

        200        210        220        230        240        250        260
KLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNN
||| : | |||  :|| :|| |||||| |||||||||| ||||||  | ||:||||||||||||||||
KLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK
610         620         630         640         650         660         670

        270        280        290        300        310        320        330
VGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQ
:||| |:  |:  ||: | || ||||::|| |||| |||||| :|: ::|||||  :|||
DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYF
```

> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-5.res made by bobryen on Thu 7 Nov 102 14:41:38 PST.

Query sequence being compared:US-09-910-186A-5 (1-1326)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-5 (1-1326) with:
File :US08123975A.seq

Sequence Name	Description	Length	Init. Score	Opt. Score	Init. Score	Sig. Score	Sig. Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	1302	1307	0.58	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	1302	1307	0.58	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	538	704	-1.15	0

1. US-09-910-186A-5 (1-1326)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score   = 1302   Optimized Score   = 1307   Significance = 0.58
Residue Identity = 98%   Matches   = 1311   Mismatches   = 15
Gaps   = 5   Conservative Substitutions =   5   = 0

```
                      x        10        20        30        40        50        60
                      GAATTCGAAACGATGGCCTCTACCTTCGGAATACATCAAGAACATCAATACCTCCATCCTGA
                                |||||  |||| |||||||||||||||||||||||||||||||||||||||||
                      CTCGAGCCATGGCTCGTCTGCTCTACCTTCCACTGAATACATCAAGAACATCAATACCTCCATCCTGA
                      X 10       20        30        40        50        60        70

                70        80        90       100       110       120       130
                ACCTGCGCTACGAATCACTGATCGACCTGTCTCGCTACCGGTTCTAAAG
                |||||||||||||||||||||||||||||||||||||||||||||||||
                ACCTGCGCTACGAATCACTCACTGATCGACCTGTCTCGCTACGGTTCTAAAG
                70        80        90       100       110       120       130       140

                140       150       160       170       180       190       200       210
                TTAACTTCGATCCGATCGACAAGAATCAGACCAGCTGTTCAATCTGGAATCGGAAGTTATCC
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTGGAATCGGAAGTTATCC
                140       150       160       170       180       190       200       210

                220       230       240       250       260       270       280
                TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGATCGTATCCCGAAAT
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                TGAAGAATGCTATCGTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGATCCGTATCCCGAAAT
                220       230       240       250       260       270       280

                290       300       310       320       330       340       350
                ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCAACTGCATGGAAAACAATTCTGGTTGGAAAG
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCAACTGCATGGAAAACAATTCTGGTTGGAAAG
                290       300       310       320       330       340       350       360

                360       370       380       390       400       410       420
                TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCA
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTTGTATTCA
                360       370       380       390       400       410       420       430

                430       440       450       460       470       480       490
                AATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                AATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
                430       440       450       460       470       480       490       500

                500       510       520       530       540       550       560       570
                TGAATAACTCCAAAATCTACATCAACACGCGCGTCTGATCGACCAGAAACGATCTCCAATCTGGGTAACATCC
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                TGAATAACTCCAAAATCTACATCAACATCTACATCAACACGCGCGTCTGATCGACCAGAAACGATCTCCAATCTGGGTAACATCC
                500       510       520       530       540       550       560       570

                580       590       600       610       620       630       640
                ACGGTTCTAATAACATCAATGTTCAAACTGGACGGTTCGTGTGACACTCACCGCTACAATCTGGATCAAATACT
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                ACGGTTCTAATAACATCAATGTTCAAACTGGACGGTTCGTGTGACACTCACCGCTACAATCTGGATCAAATACT
                580       590       600       610       620       630       640

                650       660       670       680       690       700       710
                TCAATCTGTTCGACAAAGAACTGAACGAAGAAATCAAAGACCTGTACGACAACCAGTCCAAATTCTGGTA
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                650       660       670       680       690       700       710
```

```
100-
        |
N       |
U  50-  |
M       |
B       |
E       |
R       |
        |
O  10-  |
F       |
   5-   |
S       |
C       |
O       |
R       |                              *
E       |
S       |                    *
   0-   |___|___|___|___|___|___|___|___|___|___|___|___|___|___|___
SCORE 0    145  289  434  579  723  868  1013  1157  1302
STDEV -1                         0
```

PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1.00	Joining penalty	30
Gap penalty	5.00	Window size	500
Gap size penalty	0.33		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	1047	539	441.10

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

2. US-09-910-186A-5 (1-1326) Sequence 1, Application US/08123975A
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score   = 1302   Optimized Score = 1307   Significance = 0.58
Residue Identity = 98%   Matches   = 1311   Mismatches   = 15
Gaps   =   Conservative Substitutions = 5

```
3.  US-09-910-186A-5 (1-1326)
    US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =  538    Optimized Score =  704    Significance = -1.15
Residue Identity =  55%    Matches         =  759    Mismatches   =  530
Gaps             =  71     Conservative Substitutions = 0
```

```
TGGTATCGTATTCGAAGAATACAAAGACTACTTCTTGCATCTCCAAATGTACCTGAAGGAAGTAAACGCAA
1190       1200       1210       1220       1230       1240       1250

       1250       1260       1270       1280       1290       1300       1310
ACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCT
|-|--|-|||||||||||- ||||-||||||||||| - ||-||||||| ||||||                -
ACCGTACAACCTGAAACTGGGTTGCAATTGGCAATTGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACC
1260       1270       1280       1290       1300       1310       1320       1330

1320     X
GTAAGAATTC
||| |
TCTAGAGTCGAGGCCTGCAG
    1340       1350
```

```
> O <    IntelliGenetics
O| |O
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-5-inv.res made by bobryen on Thu 7 Nov 102 14:41:54-PST.

Query sequence being compared:US-09-910-186A-5' (1-1326)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

                                                                  Init.  Opt.
Sequence Name       Description                     Length Score Score  Sig.  Frame
------------------------------------------------------------------------------------
                       **** 1 standard deviation above mean ****
 1. US-08-123-975A-6  Sequence 6, Application U 1351   55    430   1.26    0
                       **** 0 standard deviation from mean ****
 2. US-08-123-975A-4  Sequence 4, Application U 1338   44    478  -0.47    0
 3. US-08-123-975A-1  Sequence 1, Application U 1338   44    478  -0.47    0
```

Results of the initial comparison of US-09-910-186a-5' (1-1326) with: *complement*
  File :US08123975A.seq

1. US-09-910-186A-5' (1-1326)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

```
Initial Score    =  55    Optimized Score      =  430    Significance =  1.26
Residue Identity =  40%   Matches              =  519    Mismatches   =   665
Gaps             =   3    Conservative Substitutions = 89                 0
```

```
        80        90       100       110       120       130       140       150
CGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTGAACTGGTGGGAAACCGATG
                                     |||||||  ||| |||||||    ||| |||||||||
                                   ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAAATATCATCCTGAACC
                                   X          10        20        30        40        50

       160       170       180       190       200       210       220
AAACCGATATCGGTTACCATTGTTGTCCTGCAGATTCATTTTGTTAGTGATGATACCCTGGTCGTTCTTG
-       ||||||||| ||  |  | ||| |||   ||| ||| ||   |||| ||  || ||||| |
TGCGTTACAAAGACAACAATCTGATCGATCGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
  60        70        80        90       100       110       120

       230       240       250       260       270       280       290
GATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGAGTTCCAGACAGCAAGACATCTTTTCTACA
     ||||| | |||| ||| |  ||| |||  | |||| || |||| |||| |||||||||||
AACTGAATGACAAGAACCAG-TTCAAACTGACCTCTTCCGCTAACTC--------TAAGATCCGTGTAC-
  130       140       150       160       170       180

       300       310       320       330       340       350       360
CCAGCCTGAGACGCATTGGTAGCCAGACGTATTCTTGTCTTAACTACACATTGATGTATACACGATCA
||||||||||||||  ||| |||||||||||   || |||||     || ||||||||||||||||
TCAGAAATCAGAA-CATCATCTCCAACTCCGTATCCTGG-------ACTTCTCTGTTTCCTTCCACGGTATCC
  190       200       210       220       230       240

       370       380       390       400       410       420       430
TTGTTGGAACGATATTGTCCTTGTTA-CCAGACGCGTATTCTTGATGATGAATTTGGTACCACGGTACAG
|| ||| | ||| ||| || ||||   ||||||  |||| |||||| ||||  || ||||||||||||||
GTATCCCGGAAATACAAGAACGACGGTATCCATGTCCAGAATTCTTCCACAATGAATACACCATCAACTGCATGA
  250       260       270       280       290       300       310

       440       450       460       470       480       490       500
GGAAGAGTTCAGGT----AGATTGGT-AGTCATAACAGAACCACCGGACCTTTCAGGTACATGTAACCG
||||  ||||  |    ||| ||  | |||||| ||||||| ||||||| ||||| |||| ||||||||
AGAATAACTCTGGTTGGAAGATCTCCAATGCGGGTAACCGTATCATCGGAC---TCTGATCGGATATCAACG
  320       330       340       350       360       370       380

       510       520       530       540       550       560       570
CGGATACCTACATTGTTGACGTGCAACGTATTTGTTCGGATCGTACAGATTCAGCAGTCGTAGTACGGTTTCGTCCG
|||||||   || ||  ||||||| |||  || ||| |||  ||  ||| |||| |  ||||||| |||||||||
GTAAGACCAAATCTGTATTCTTCGA-ATACAACATCCGTGAAGACA---TCTCTGAATACATCAATCCGCGCTGG
  390       400       410       420       430       440       450

       580       590       600       610       620       630       640
TACTGGCAGGTAGTCACCCCAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCGTACAGGTCTTTGATT
||||   ||| ||||||||  ||| | | ||||| |||||  || ||  ||||||||| ||||||  |||||||
TTCTTC--GTTACCATCACCAATAACCTGAACATGCTAAAATCTACATCAACGGTAAACTGGAAATCTAATA
  460       470       480       490       500       510       520

       650       660       670       680       690       700       710
TCTTTTTGTTCAGTTC-----TTTGTGAACAGATTGAA---GTATTTGATCCAGATGTAGCCGTGAGTG
||||  |||||  |         |  |||  ||| ||    |||||| || |||| | ||||||  ||||
CCGACACCAAAGACATCCGTGAAGTTATCGCTGAAGTTAATCAATCTTCAAACTGGACATCGGACGGTGACATCGGATC
  530       540       550       560       570       580       590

       720       730       740       750       760       770
TCACGACAACCGTCCAGTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAG-----ATTGGAGATC
```

```
100-|
    -
    -
    -
  N -
  U -
 50-|
  M -
  B -
  E -
  R -
    -
  O -
  F -
 10-|
    -
    -
  S -
  E 5-|
  Q -
  U -
  E -
  N -
  C -                                              *
  E -
  S -                                         *
   0-+----|----|----|----|----|----|----|----|----|----|----|
SCORE 0   |16   |12   |18   |24   |31   |37   |43   |49   |55
STDEV -6   -5   -4   -3   -2   -1    0    1
```

```
          PARAMETERS

Similarity matrix    Unitary
Mismatch penalty     1           K-tuple            4
Gap penalty          5.00        Joining penalty   30
Gap size penalty     0.33        Window size      500
Cutoff score         1
Randomization.group  0

          SEARCH STATISTICS

             Mean    Median    Standard Deviation
Scores:       47       45            6.35

             CPU                     Total Elapsed
Times:     00:00:00.00              00:00:00.00

Number of residues:          4027
Number of sequences searched:   3
Number of scores above cutoff:  3
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

2. US-09-910-186A-5' (1-1326) Sequence 4, Application US/08123975A
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score	=	44	Optimized Score	=	478
Residue Identity	=	43%	Matches	=	582
Gaps	=	78	Conservative Substitutions	=	78

Significance = -0.47
Mismatches = 681

3. US-09-910-186A-5' (1-1326)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

```
Initial Score        =   44    Optimized Score        =   478    Significance  =  -0.47
Residue Identity     =   43%   Matches                =   582    Mismatches    =   681
Gaps                 =         Conservative Substitutions =  78                   0
```

GGGGTGAACGT
1310

Thu Nov 7 14:52:51 2002

```
| |||| | | ||| | | | | || | | ||| | || ||| | | |  | ||| | |   | ||| ||
TAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACA-
   1170      1180      1190      1200      1210      1220      1230

   1270      1280      1290      1300      1310      1320          X
GATGGAGGTATTGATGATGTTCTTGATGTATTCAGTGAAGGTAGAGGCCATCGTTTCGAATTC
 ||-|--|| | | |||||| |  | ||-|| || |-|   | | ||-| |   |    |
-ATCGTCAGATCGA--ACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTT
   1240      1250      1260      1270      1280      1290      1300

GGGGTGAACGT
   1310
```

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-6.res made by bobryen on Thu 7 Nov 102 14:32:29-PST.

Query sequence being compared:US-09-910-186A-6 (1-435)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

   Results of the initial comparison of US-09-910-186A-6 (1-435) with:
        File :US08123975A.pep
```

```
100-

 N -
 U -
 M 50-
 B -
 E -
 R -

   -
   -
 O -
 F 10-

 S -
 E  5-
 Q -
 U -
 E -
 N -
 C -
 E -
 S  0---|---|---|---|---|---|---|---|---|---|---|---|---
               *  *                        *           *
 SCORE  0   46   92  139  185  231  277  324  370  416
 STDEV     -1   -1    |    |    |    |    |    |    |
                                             1    1
```

```
                    PARAMETERS

Similarity matrix      PAM-150     K-tuple             1
Threshold level of sim. 16%       Joining penalty
Mismatch penalty        1         Window size        20
Gap penalty             5.00                         435
Gap size penalty        0.05
Cutoff score            1
Randomization group     0

                SEARCH STATISTICS

Scores:      Mean      Median    Standard Deviation
             263       181       132.66

             CPU
Times:    00:00:00.00            Total Elapsed
                                 00:00:00.00

Number of residues:                1704
Number of sequences searched:         3
Number of scores above cutoff:        3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
Sequence Name    Description                                              Length  Init. Opt.
                                                                                  Score Score  Sig. Frame
--------------   -----------                                              ------  ----- -----  ---- -----
                 ****     1 standard deviation above mean ****              416    416   416   1.15   0
1. US-08-123-975-3   Sequence 3, Application U                             415    416   416   1.15   0
                 ****     0 standard deviation from mean ****               416
2. US-08-123-975A-5  Sequence 5, Application U                             439    193   273  -0.53   0
3. US-08-123-975A-2  Sequence 2, Application U                             850    180   275  -0.63   0
```

```
1. US-09-910-186A-6 (1-435)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    = 416   Optimized Score       =  416   Significance =  1.15
Residue Identity = 100%  Matches               =  415   Mismatches   =    0
Gaps             =   0   Conservative Substitutions =  0

              10        20        30        40        50        60        70
   MASTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
   X          10        20        30        40        50

              80        90       100       110       120       130       140
   YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI
              60        70        80        90       100       110       120

             150       160       170       180       190       200       210
   NISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   NISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
             130       140       150       160       170       180       190

             220       230       240       250       260       270       280
   ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTNIY
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTNIY
   200       210       220       230       240       250       260

             290       300       310       320       330       340       350       360
   LNSSLYRGTKFIIKKYASGNKDNIVRNNDRVIINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   LNSSLYRGTKFIIKKYASGNKDNIVRNNDRVIINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
   270       280       290       300       310       320       330       340

             370       380       390       400       410       420       430
   VMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGE
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   VMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGE
   350       360       370       380       390       400       410

   X
   RPL
   | | |
   RPL
   X
```

```
2. US-09-910-186A-6 (1-435)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    = 193   Optimized Score       =  273   Significance = -0.53
Residue Identity = 38%   Matches               =  169   Mismatches   =  230
Gaps             =  17   Conservative Substitutions = 26

              10        20        30        40        50        60        70
   MASTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
   |||      ::   : |:  |  :  |||||  :|:::|||:::::  |::: :  :  :::
   FNKYNSEILNNILNLRKDNLIDLSGYGAKVEVYDGVELN--DKNQFKITSSANSKIRVTQNQNII
   X          10        20        30        40        50        60
```

```
                680       690       700       710       720       730       740

     340       350       360       370       380       390       400
QAGVEKILSALEIPDVGNLSQVVVMKSKNDQGI-TNKCKMNLQDNGNDIGFHQFNNIAKLVA------
                                  :   |||   |    |   :||  | |||| :
-FKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYF
     750       760       770       780       790       800       810

     410       420       430 x
--SNWYNRQIERS--SRTLGCSWEFIPVDDGWGERPL
  :||  |::    |||| ||||||||||||
CISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
     820       830       840       850
```

```
     80        90       100       110       120       130       140
YNSMYENFSTSFWIRIPKYFNSIS---LNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYS
::|: ||  |||||||||||     |||||||||||:::     ||||| ||   |
FNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTILIDINGKTIKSVFFEYN
     70        80        90       100       110       120       130

    150       160       170       180       190       200       210
QMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNL
 |  |:|||||| ||||||| |||:||||| ||  :             :|||||  ||  ||||| ||||:|
IREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSI
    140       150       160       170       180       190       200

    220       230       240       250       260       270       280
FDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYDVNVGIRGYMYLKGPRGSVMTT
|:  |:  ::   ||: :   ||||||| |:   |||| | |   ||:   |||||| ||||||||||  ||
FNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMENAGNKNSYIKLKKDSPVGEILTRSKYNQNSKY
    210       220       230       240       250       260       270       280

    290       300       310       320       330       340       350
NIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVKNKEYRLATNASQAGVEKILSALEIPDVGNLS
||  |:  |   ||||::  :|:|:||||: :|||  :   ||||:     ::
INYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFY
    290       300       310       320       330       340       350

    360       370       380       390       400       410
QVVVMKSKNDQGI-TNKCKMNLQDNGNDIGFHQFNNIAKLVA------SNWYNRQIERS--SRTLG
:   |||  :   |      |   |  |||||:||    |        :||  |:: |||||
NTQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYEBSGIVFEEYKDYFCISKWYLKEVKRKPYNLKLG
    360       370       380       390       400       410       420

    420       430 x
CSWEFIPVDDGWGERPL
|:|:||||||||
CNWQFIPKDEGWTE
         x
```

3. US-09-910-186A-6 (1-435)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

```
Initial Score     = 180   Optimized Score = 275   Significance = -0.63
Residue Identity  = 37%   Matches         = 233   Mismatches    = 169
Gaps              = 17    Conservative Substitutions = 27
```

```
     x         10        20        30        40        50
                MASTFFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQ
                    ::|   |  ||||||:|||||::  :  ||:: :|::    | :
NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELN--DKNQ
    390       400       410       420       430       440       450

     60        70        80        90       100       110       120
IQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSIS---LNNEYTIINCMENNSGWKVSLNYGE
      |:    :    ||:   ||  |||||||||||     |||||||||||| ||||||| :| ||
FKLTSSANSKIRYTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNR
    460       470       480       490       500       510       520

    130       140       150       160       170       180       190
IIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIM
||||| :|   |: ||||:|  | |:|||||| ||||||| |||:||||| ||  :  |  |  :  ||  ||
IIWTLIDINGKTIKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEII
    530       540       550       560       570       580       590       600

    200       210       220       230       240       250       260
FKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYDVN
||||| :||  ||| ||||:| :  |:  ::   ||: :   ||||||| |:   |||| |  :   ||:
FKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMENAGNKKNSYIKLK
    610       620       630       640       650       660       670

    270       280       290       300       310       320       330
NVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVKNKEYRLATNAS
  |||||| ||||||||  || ||  |:  |   ||||::  :|:|:||||: :|||  :   ||||:
KDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKY
```

```
> O <
O|lO  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-7.res made by bobryen on Thu 7 Nov 102 14:42:16-PST
```

```
Query sequence being compared:US-09-910-186A-7 (1-1341)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

Results of the initial comparison of US-09-910-186A-7 (1-1341) with:
       File :US08123975A.seq
```

```
                                                                  Init. Opt.
Sequence Name    Description                        Length Score Score  Sig. Frame
-------------    -----------                        ------ ----- -----  ---- -----
                           **** 1 standard deviation above mean ****
1. US-08-123-975A-6  Sequence 6, Application U  1351 1320  1323   1.16  0
                           **** 0 standard deviation from mean ****
2. US-08-123-975A-4  Sequence 4, Application U  1338  533   699  -0.58  0
3. US-08-123-975A-1  Sequence 1, Application U  1338  533   699  -0.58  0
```

```
1. US-09-910-186A-7 (1-1341)
   US-08-123-975A-6  Sequence 6, Application US/08123975A

Initial Score    =   1320    Optimized Score    =   1323    Significance =   1.16
Residue Identity =   1320    Matches            =   1323    Mismatches   =     12
Gaps             =      0    Conservative Substitutions =      0         Gaps   =      0
```

```
        X 10        20        30        40        50        60        70
GAATTCACGATGCCAACAAATACAATTCCGAACAATATCATCCTGAACAATCCTGCGTTACAAAGAC
  -  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  - ATGGCTTCAACAAATACAATTCCGAACAATCCTGAACAATCATCCTGAACCTGCGTTACAAAGAC
  X        10        20        30        40        50        60

        80        90       100       110       120       130       140
AACAATCTGATCGATCGTCTCGGTTACGGTGCTAAAGTTGAAGTTACGACGGTGTTGAACTGAATGACAAG
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AACAATCTGATCGATCGTCTCGGTTACGGTGCTAAAGTTGAAGTTACGACGGTGTTGAACTGAATGACAAG
       70        80        90       100       110       120       130

       150       160       170       180       190       200       210
AACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAAC
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAAC
      140       150       160       170       180       190       200       210

       220       230       240       250       260       270       280
TCCGTATCCTGGACTTCTCTGTTCCTTCGTTTCCTTCTGGATCCGTATCCCGAAAATACAAGAACGACGGTATCCAGAAT
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCCGTATCCTGGACTTCTCTGTTCCTTCGTTTCCTTCTGGATCCGTATCCCGAAAATACAAGAACGACGGTATCCAGAAT
      220       230       240       250       260       270       280

       290       300       310       320       330       340       350       360
TACATCCACAATGAATACACCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCTCCATCCGCGGT
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TACATCCACAATGAATACACCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCTCCATCCGCGGT
      290       300       310       320       330       340       350

       370       380       390       400       410       420       430
AACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGATTCTTCGAATACAACATCCGT
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGATTCTTCGAATACAACATCCGT
      360       370       380       390       400       410       420

       440       450       460       470       480       490       500
GAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGCTAAAATC
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGCTAAAATC
      430       440       450       460       470       480       490

       510       520       530       540       550       560       570
TACATCAACGGTAAACTGGAATCTAATACCGACAATCAAAGACATCCTGAAGTTATCCGTAACGGTGAAATC
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TACATCAACGGTAAACTGGAATCTAATACCGACAATCAAAGACATCCTGAAGTTATCCGTAACGGTGAAATC
      500       510       520       530       540       550       560       570

       580       590       600       610       620       630       640
ATCTTCAAACTGACGCGGTGACATGGACTGACTGACTGATGGATGAAATACTTCTCCATCTTCAACACC
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCTTCAAACTGACGCGGTGACATGGACTGACTGACTGATGGATGAAATACTTCTCCATCTTCAACACC
      580       590       600       610       620       630       640

       650       660       670       680       690       700       710       720
GAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCGGTACCCAGTCTTACTCCGAATACCTGAAAGACTTCTGG
```

```
100-
    -
    -
N 50-
U   -
M   -
B   -
E   -
R   -
    -
O   -
F 10-
    -
S   -
E  5-
Q   -                                              *
U   -
E   -
N   -
C   -                                                                        *
E   -
S  0-
   0 ----|----|----|----|----|----|----|----|----|----|----|----|----|----|
        147  293  440  587  733  880 1027 1173 1320
SCORE 0  |    |    |    |    |    |    |    |    |
STDEV -1
```

```
           PARAMETERS
Similarity matrix    Unitary   K-tuple            1
Mismatch penalty        1      Joining penalty   30
Gap penalty          5.00      Window size      500
Gap size penalty     0.33
Cutoff score            1
Randomization group     0
```

```
           SEARCH STATISTICS
           Mean    Median       Standard Deviation
Scores:     795      534               454.37

           CPU                  Total Elapsed
Times:  00:00:00.00             00:00:00.00

Number of residues:          4027
Number of sequences searched:   3
Number of scores above cutoff:  3
```

```
The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

2. US-09-910-186A-7 (1-1341)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 533	Optimized Score = 699	Significance = -0.58	
Residue Identity = 55%	Matches = 754	Mismatches = 535	
Gaps = 71	Conservative Substitutions = 0		

```
ACAAGAACACGGTATCCAGAATTACACCACAAATGAATACCATCACCATCACTGATGAGAATAACTCTG
||  |||  |  |                     ||||||||||  |  |||  || || |||   ||
ACTTCAACTCC------ATCTTCTGAACAATGAATACACCACCATCACTGACATGGAAAACAATTCTG
         290                           300        310        320        330        340        350

GTTGGAAGATCTCCATCCGCGGTAACCGTATACCGACTTC--AAGAAGAAGAAGAAGCTTTTCCTGGCTCCG
  |  |||||  ||  |||| |   || |         |||    |  |||  ||  |||| |||| ||||
GTTGGAAGTTATCTGAACTGGATCTTGATCGATATCAACGCTGAAGGTCCGCGTG
340        350        360        370        380        390        400

AGAAATGAAGAATACCGTCT---GGCTACCAAGTGCTGTGTAGAAAGAGATCTTGTCTGCTCTG
||| |  |||||||     ||||    ||||  |||| | ||| ||||| ||  ||| | |||
GTTGAAAGTGATATCTTGACTCTGACTGATCATCTGACTCTGCAGGACTCAGGACACTCAGGAAAATCAAAACAGCGTG
1000       1010       1020       1030       1040       1050       1060
                         360        370        380        390        400        410        420
```

3. US-09-910-186A-7 (1-1341) Sequence 1, Application US/08123975A
   US-08-123-975A-1 Sequence 1, Application US/08123975A

```
                 X       10        20        30        40        50
Initial Score   =  533   Optimized Score  =   699   Significance  =  -0.58
Residue Identity =  55%   Matches          =   754   Mismatches    =   535
                         Conservative Substitutions = 71   Gaps = 0
```

```
TAAGAATTC
CCGCTGTAACCCGGGAAAGCTT
1320   X 1330
       1340
```

```
    |  |  ||      |||     | |       |  ||        | |||||  |||||| ||||||| ||||| ||
AACAAATGCAAAATGAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAAC
   1140        1150        1160        1170        1180        1190        1200

1190      1200        1210        1220        1230        1240        1250      1260
GAATCTGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAA
   |  |||||                        | |         |||| ||||||      |  |
AA------TATCG-------CTAAACTGGTTGCT--------TCCAACTGGTAC------AATCGTCAG
         1210        1220              1230                  1240

    1270        1280        1290        1300        1310        1320        1330
CGCAAACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGACCGAATAG
   |  |||   | |     | ||||||||||   ||||  |||||||||||       |  | |||||       ||
ATCGAACGTTCCTCTCGCACTCTCGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGT
   1250        1260        1270        1280        1290        1300        1310

    1340
TAAGAATTC
    |
CGGCTGTAACCCGGGAAAGCTT
   1320   X 1330
```

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-7-inv.res made by bobryen on Thu 7 Nov 102 14:42:32-PST.

Query sequence being compared:US-09-910-186A-7' (1-1341)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

Results of the initial comparison of US-09-910-186A-7' (1-1341) with:
        File:US08123975A.seq
```

complement

```
PARAMETERS

Similarity matrix    Unitary
Mismatch penalty         1        K-tuple              4
Gap penalty           5.00        Joining penalty     30
Gap size penalty      0.33        Window size        500
Cutoff score             0
Randomization group      0

SEARCH STATISTICS

Scores:          Mean       Median       Standard Deviation
                  46          44              6.35

Times:            CPU                       Total Elapsed
              00:00:00.00                   00:00:00.00

Number of residues:                4027
Number of sequences searched:         3
Number of scores above cutoff:        3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                        Init.  Opt.
Sequence Name   Description            Length  Score  Score  Sig.  Frame
--------------  --------------------   ------  -----  -----  ----  -----
                **** 1 standard deviation above mean ****
1. US-08-123-975A-6 Sequence 6, Application U  1351    54    488   1.26     0
                **** 0 standard deviation from mean ****
2. US-08-123-975A-4 Sequence 4, Application U  1338    43    481  -0.47     0
3. US-08-123-975A-1 Sequence 1, Application U  1338    43    481  -0.47     0

1. US-09-910-186A-7' (1-1341)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score   =    54    Optimized Score       =   488    Significance  =  1.26
Residue Identity =  418    Matches               =   563    Mismatches    =   716
Gaps             =   90    Conservative Substitutions =                     0

                   X        10        20        30        40
              GAATTCTT--ACTATTCGGTCC--AACCTTCGTCTTTCGGGATGAACTGCCA
              CTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGACAACAATCTGA
               10   20   X   30        40        50        60        70

              50        60        70        80        90       100       110
              AATTGCAACCCAGTTCAGGTTGTACGGTTTGCGTTTA--ACTTCCTTCA--GGTACCATTTGGAGATGCAGA
              80        90       100       110       120       130       140

              TCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGGGTGTTGAACTGAATGACAAGAACCAGTTCA
              120       130       140       150       160       170       180
              AGTAGTCTTTGTATTCTTCGAATACATACCAGATTCGTAGAAACGGTGGATACCGATCAGAGACCGATTCGT

              AACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAACTCCGTATTCC
              150       160       170       180       190       200       210       220
              190       200       210       220       230       240       250
              CAGTAGATTCTTCATCTTCTTCTGAACAGCAGCTGGCAAGTAGTCGGCTGTTCGTCGTTGTATTCTTT-----

              TGGACTTCTCGTGTTCCTTCGTGGATCCGTATCCCGAAAATACAAGAACGACGGTATCCAGAATTACATCCACA
              230       240       250       260       270       280       290
              260       270       280       290       300       310
              --------GATCTGAGATGGTGTTGTAGAGTTCGTGCGGAATCAGAGATC--GGAGCCAGGAAAAAGCTTTTCT

              ATGGAATACACCATCATCAACTGCATGAAGAATAAACTCTGGTTGGAAGATCTCCATCCGCGGTAACCGTATCA
              300       310       320       330       340       350
              320       330       340       350       360       370
              TCTTCTTTCTTGAAGTACTTGTAGGTGTATACGGCCATTCCGTGATTCA--------GGTTGAAGAAGTCC

              TCTGGACTCTGATCGATATCAACGGTAAGACCGTAAGACCAAATCGTATTCTTCGAATACAACATCCGTGAAGACATCT
              370       380       390       400       410       420       430
              380       390       400       410       420       430       440
              AGGTAGAGTGTAGTCTTCTTTACGTACGATGTCATCATTGATCGGACTG---AGAGTTAGATTTGCGACGGATG

              CTGAATACAATCAATCGCTCGGTTGGTCTTCGTTCGTTACCATTCACCAATAACCTGAACAATGCTAAAATCTACATCAACG
              440       450       460       470       480       490       500
              450       460       470       480       490       500       510       520
              ATGAACTTTCACCGATGTACAGGTCGCGGTAGTTGATGTATTTAGAGTTCTGGTTGTATTTGGAACGAGTC

              GTAAACTGGAATCGAATCGATCAACAAAGACATCCGTAAGGTTGATCATCTTCAACATCTTCAACATCT
              510       520       530       540       550       560       570       580
              530       540       550       560       570       580       590
              AGGATTCACCAACCGGAGAGTCTTTCTCAGTTGATGTAAGAGTTCTTGTTACCAGCATTGAACATATAG

              TGGACGGTGAC-ATCGATCGTACCACCAGTTCATCTGATGAAATACTTCT-----CCATCTTCAACACCGAA
              590       600       610       620       630       640
              600       610       620       630       640       650       660
              TATTCTTTGTTGTACATCAGCGGATTACCCCAGA--AGTCTTTCAGGTATTCGGAGTAAGACTGATCTTG
```

SCORE   0   6   12   18   24   30   36   42   48   54
STDEV -6 -5 -4 -3 -2 -1   0   1

100-
    -
 N -
 U 50-
 M -
 B -
 E -
 R -
    -
 O 10-
 F -
    -
 S 5-
 E -
 Q -
 U -
 E -
 N -
 C -
 E -
 S -
    0-

2. US-09-910-186A-7' (1-1341)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 43   Optimized Score = 481   Significance = -0.47
Residue Identity = 42%   Matches = 716   Mismatches = 577
Gaps = 79   Conservative Substitutions = 0

3. US-09-910-186A-7' (1-1341)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score   = 43   Optimized Score = 481   Significance = -0.47
Residue Identity = 42%   Matches   = 716   Mismatches   = 577
Gaps   =   Conservative Substitutions = 79

```
|||| ||   || |||  |  | | ||  | ||    | ||   |||  |||| ||  |   | |||| |  | | |||   |  |||||
GTGTAGAAAAGATCTTGTCTCGCTCGGAAATCCCGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAAT
   1040        1050        1060        1070        1080        1090        1100

                                                          1170        1180
   1120        1130        1140        1150        1160
CCAGGAATACGGAGTTGAAGATGATGTTCTG-ATTCTGAGTAACACGGATCTTAGAGTTAGCGGAAGAGGTC
|||| ||||    || |||||     | ||    ||    | | |||| |   ||  |  ||| |||   |||
CCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTT
   1110        1120        1130        1140        1150        1160        1170

   1190        1200        1210        1220        1230        1240        1250
AGTTTGAACTGGTTCTTGTCATTCAGTTCAACACCGTCGTATACTTCAACTTAGCACCGTAACCAGGACAGA
 |   ||  |   | |  |||    |  ||   |||  ||  | | |||||    ||  ||||||| ||
TCATCGGTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAAC--TGGTACAATCGTCAGATCGA
  1180        1190        1200        1210        1220        1230        1240

   1260        1270        1280        1290        1300        1310        1320
TCGATCAGATTGTTGTCTTTGTAACGCCAGTTCAGGATGATATTGTTCAGGA--TTTCGGAATTGTATTTGT
||| ||   |||  | |  | |  |    || |   | ||    || || |   | ||   | || ||   |
ACGTTCCTCTCGCACTCTGGGTTGCTCTTG-GGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGC
  1250        1260        1270        1280        1290        1300        1310        1320

   1330        1340
TGGCCATCGTGAATTC
|| | ||| |  |||
TGTAACCCGGGAAAGCTT
   1330          X
```

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-8.res made by bobryen on Thu 7 Nov 102 14:32:54-PST.

Query sequence being compared:us-09-910-186a-8 (1-440)
Number of sequences searched:        3
Number of scores above cutoff:       3

Results of the initial comparison of us-09-910-186a-8 (1-440) with:
   File : US08123975A.pep
```

```
Sequence Name      Description                                    Length  Init. Opt.
                                                                          Score Score   Sig. Frame

1. US-08-123-975A-2  Sequence 2, Application US/08123975A  U  850  439  439   0.58   0
2. US-08-123-975A-5  Sequence 5, Application U              439  438  438   0.58   0
                     **** 1 standard deviation below mean ****
3. US-08-123-975A-3  Sequence 3, Application U              415  189  259  -1.15   0
```

```
1. US-09-910-186a-8 (1-440)
   US-08-123-975A-2  Sequence 2, Application US/08123975A

Initial Score     = 439   Optimized Score         = 439   Significance  = 0.58
Residue Identity  = 99%   Matches                 = 438   Mismatches    = 2
Gaps              =        Conservative Substitutions =  0                   = 0
```

```
                   X          10         20         30         40         50
            MANKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTS
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
            LKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTS
            400        410        420        430        440        450        460

                   60         70         80         90        100        110        120
            SANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKKNDGIQNYIHNEYTIINCMKKNNSGWKISIRGNRIIWTL
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            SANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKKNDGIQNYIHNEYTIINCMKKNNSGWKISIRGNRIIWTL
            470        480        490        500        510        520        530

                  130        140        150        160        170        180        190
            IDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGD
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            IDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGD
            540        550        560        570        580        590        600

                  200        210        220        230        240        250        260
            IDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVG
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            IDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVG
            610        620        630        640        650        660        670

                  270        280        290        300        310        320        330        340
            EILTRSKYINQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEE
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            EILTRSKYINQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEE
            680        690        700        710        720        730        740        750

                  350        360        370        380        390        400        410
            KLFLAPISDSDELYNTIQIKEYDEQPYYSCQLLFKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWY
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            KLFLAPISDSDEFYNTIQIKEYDEQPYYSCQLLFKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWY
            760        770        780        790        800        810        820

                  420        430        X
            LKEVKRKPYNLKLGCNWQFIPKDEGWTE
            ||||||||||||||||||||||||||||
            LKEVKRKPYNLKLGCNWQFIPKDEGWTE
            830        840        850
```

```
2. US-09-910-186a-8 (1-440)
   US-08-123-975A-5  Sequence 5, Application US/08123975A

Initial Score     = 438   Optimized Score         = 438   Significance  = 0.58
Residue Identity  = 99%   Matches                 = 437   Mismatches    = 2
Gaps              =        Conservative Substitutions =  0                   = 0
```

```
                   X          10         20         30         40         50         60         70
            MANKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVF
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVF
            X          10         20         30         40         50         60         70
```

```
                                           PARAMETERS

Similarity matrix  PAM-150       K-tuple                    1
Threshold level of sim.  168     Joining penalty           20
Mismatch penalty    1            Window size              440
Gap penalty         5.00
Gap size penalty    0.05
Cutoff score        0
Randomization group 0
```

```
                                     SEARCH STATISTICS

                   Mean      Median    Standard Deviation
Scores:            355       190       144.05

                   CPU                 Total Elapsed
Times:             00:00:00.00         00:00:00.00
```

```
Number of residues:          1704
Number of sequences searched: 3
Number of scores above cutoff: 3
```

```
The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
100-

  -
N -
U -
M 50-
B -
E -
R -

  -
O -
F 10-

  -
S -
E 5-
Q -
U -
E -
N -
C -
E -                                    *                        *
S 0 -|---------|---------|---------|---------|---------|---------|---------|
SCORE  0    49    98   146   195   244   293   341   390   439
STDEV -1    -1                *
```

```
            360       370       380       390       400       410       420
     QIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNW
     :|::| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|: |||
     VMKSKNDQGI-TNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVA-------SNWYNRQIERS--SRTLGCSW
          350       360       370       380            390       400

     430       440
     QFIPKDEGWTE
     ||::|:||
     EFIPVDDGWGERPL
     410 X
```

```
            80        90        100       110       120       130       140
     LDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDI
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     LDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDI
            80        90        100       110       120       130       140

          150       160       170       180       190       200       210
     SEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     SEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS
          150       160       170       180       190       200       210

          220       230       240       250       260       270       280
     QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDL
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDL
          220       230       240       250       260       270       280

          290       300       310       320       330       340       350       360
     YIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDELYNTIQIK
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     YIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIK
          290       300       310       320       330       340       350

          370       380       390       400       410       420       430
     EYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFI
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     EYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFI
     360       370       380       390       400       410       420       430

     440
     PKDEGWTE
     ||||||||
     PKDEGWTE
     X
```

```
3. US-09-910-186A-8 (1-440)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =   189  Optimized Score    =   259  Significance    =  -1.15
Residue Identity =   38%  Matches            =   162  Mismatches      =   221
Gaps             =   17   Conservative Substitutions   =    26
```

```
            10        20        30        40        50        60        70
     MANKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNS
                       :::|:  : :          |||
                       RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNS
                       X        10        20        30        40        50

            80        90        100       110       120       130       140
     VFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRE
      :  |:|||||||||||||||| ||||| |:     ||||::: ||:: |||||||||:|:||:|:::|:
     MYENFSTSFWIRIPKYFNSIS---LNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKKYSQMI
            60        70        80        90        100       110       120

          150       160       170       180       190       200       210
     DISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT
      |::|::||| ||| |||: :||||:: ||  :||:|| | | ||| ||: || |||| :|||||:|:||
     NISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
          130       140       150       160       170       180       190

          220       230       240       250       260       270       280
     ELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINY
     ||: |: : |||| ||: |||  |||  ||  :|  :|      |||: :|:|  | :: ||||||:
     ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTNIY
          200       210       220       230       240       250       260

          290       300       310       320       330       340       350
     RDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDELYNTI
      :       ||||:|:|:: :| ||:::|::     |||: :: :::   ||:  |:  | : ::
     LNSSLYRGTKFIIKKYASGNKDNIVRNNDRVIINVVVKNKEYRLATNASQAGVERILSALEIPDVGNLSQVV
          270       280       290       300       310       320       330       340
```

```
> O <
O|O Intelligenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-9.res made by bobryen on Thu 7 Nov 102 14:42:59 PST

Query sequence being compared:US-09-910-186A-9 (1-1371)
Number of sequences searched:           3
Number of scores above cutoff:          3

    Results of the initial comparison of US-09-910-186A-9 (1-1371) with:
    File :US08123975A.seq
```

```
100-
    -
    -
N   -
U 50-
U   -
M   -
B   -
E   -
R   -
    -
O   -
F 10-
    -
S   -
E  5-
Q   -
U   -
E   -
N   -
C   -
E   -
S  0-------------------------------------------------------------------*-----
                 |    |    |    |    |    |    |    |    |    |    |    |    |
SCORE 0   37    74   110  147  184  221  257  294  331
STDEV    -4    -3        -2   -1         0         1
```

```
            PARAMETERS
Similarity matrix    Unitary     K-tuple                 4
Mismatch penalty        1        Joining penalty        30
Gap penalty          5.00        Window size           500
Gap size penalty     0.33
Cutoff score            1
Randomization group     0

            SEARCH STATISTICS
                  Mean    Median     Standard Deviation
Scores:           270      241            52.54

                  CPU                Total Elapsed
Times:      00:00:00.00              00:00:01.00

Number of residues:            4027
Number of sequences searched:     3
Number of scores above cutoff:    3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                                Init.  Opt.
Sequence Name   Description                       Length Score  Score  Score  Sig.  Frame
-------------   -----------                       ------ -----  -----  -----  ----  -----
                **** 1 standard deviation above mean ****
1. US-08-123-975A-6 Sequence 6, Application U 1351  331    618    1.16    0
                **** 0 standard deviation from mean ****
2. US-08-123-975A-4 Sequence 4, Application D 1338         240    620   -0.57    0
3. US-08-123-975A-1 Sequence 1, Application U 1338         240    620   -0.57    0
```

```
1. US-09-910-186A-9 (1-1371)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score  =  331    Optimized Score   =  618   Significance  =  1.16
Residue Identity = 50%   Matches           = 706    Mismatches    =  545
Gaps             =        Conservative Substitutions = 138
```

```
        40         50         60         70         80         90        100
ACACCAACAACTCCCCTGTTGAAGGACATCATCAACAACGAGTACTTCAACAACATCAACGACTCCAAGATCCTGT
                       |||   |||||  |||| ||| ||||| |  |||||| ||   |||  |||||||
                       ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAA--TATCATCCTGA
                       x          10         20         30         40

110        120        130        140        150        160        170        180
CCCTGCAGAACCGTAAGAACACACCTTGTCGACACCTCCGGTTACAACGCCGAGGTCTCCGAGGAGGTGACG
|||||   |||| |||||| |||||  ||||| | |||||  ||| || ||||| ||||||||||||||||
ACCTGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTCTAAAGTTGAAGTTGAAGTATACGACGGTG
50         60         70         80         90        100        110        120

190        200        210        220        230        240        250
TCCAGTCGACCCAATCTTCCATTCGACTTCAAGCCTGGGTTCCTCCGGTGAGGACAGAGGTAAGGTCATCG
  |||||||   |||||||||  ||| |||||||     |||||| |||||   ||| |  ||| |||||||
TTGAACTGAATGACAAGAACC-----AGTTCAAACTGACCTCTTCCGCT-----AACTCTAAGATCCGTG
130        140                 150                160        170        180

260        270        280        290        300        310        320
TCACCCAGAACGAGAACATCGTCTACAACTCCATGTACGAGTCCTTCTCCCATCCTTCTGGATCAGAATC-
|||||||| |||||  |||||| ||||||||||  ||  ||| ||||||||||| |||||||||||||||| |||
TTTACTCAGAATCAGAAACATCATCTTCAACTCCGTATTCCTGGACTTCCTGGACTTCTGGATCCGGATCCGATCC
190        200        210        220        230        240        250

330        340        350        360        370
AACAAGTGGGTCTCCAACTTGCCA-------GGTTACACCATCATCGACTCCGACTCCGTCAAGAACCA
  ||||   |||||||||||||||        |||| ||||||||||||||||||||||||||||||||||
CGAAATACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAAGATA
260        270        280        290        300        310        320

380        390        400        410        420        430        440        450
ACTCCGGTTGGTCCATGGTATCATCTCCAACTTCCTGGTCTTCACCCTGAACGAGAAGAGGAGGACTCCGAGC
||||| |||||  ||||||| ||||| |||||| |||||   ||| ||||||| |||||||| ||||| |||||
ACTTGGTTGGAAGATCTCCATCCGCGTAACCGTAATCATCTGGGACTCTGGATATCATCGATATCAACGGTAAGACCA
330        340        350        360        370        380        390

460        470        480        490        500        510        520
AGTCCATCAACTTCTCTACGACATCTCCAACGAACCGTCTCGGTTACAACAA--GTGGTTCTTGTCACCG
 ||| ||||||||||| ||| ||  ||||  |||  ||| |||  |||||||||||   ||||| ||||||||
AATCTGTATTCTTCGAATACAACAACCGTGAAGACATCTCTGAAATCTCTGAATACAATCGCTGGTTCTTCGTTACCA
400        410        420        430        440        450        460

530        540        550        560        570        580        590
TCACCAACAACATGATGGGTAACATGGGTAACATGAGAGATCTACATCAACGGTAACGGTAGCTGACCACCATCAAGGTCAAGG
||||||| || ||  ||| |    ||    |||  ||||   | |||||||| |  ||| ||  |||||||||||||
TCACCAATAACCTGA--ACAATGCTAAAAATCTACATCAACGGTAAACTGAAATCAACGGTAACTACCGACATCGTACCC
470        480        490        500        510        520        530

600        610        620        630        640        650        660
AGTTGACCGGTATCAACTTCTCCAAGACCATCACCTTCGAGATCAACAACAAGATCCCAGACACCGGTCTGATCA
||   ||  ||||||||||||||||||  ||| ||    || || |  |  |||| || |||| ||||||||||||
ACATCCGTGAAGTTATCGCTAACGGTGAAATCAGCT------TCAAACTGACGGTGACATCGACTCGTACCCC
540        550        560        570        580        590        600

670        680        690        700        710        720        730
CCTCCGACTCCGACAACATCAACAATGTGGATCCGTGACTTCTACAATCTTCCGCCAAGGAGTTGGACGGTAAGG
```

```
                                              CCATTCAACATCTTCCTCACCACCAACAACTCCCTGT-TGAAGGACATCATCAACGAGTACTTCAACACAT
                                              ||||| ||||||||||  ||| |||||||||||||||  ||| |||||||| ||||| || |||||||||
                                              CTCGAGCCATGGCTCGTCTGCTGCTTCCATCTTCAACACCTTCACTGAATACATCAAGAACAT
                                                      x        10        20        30        40        50        160

         90       100       110       120       130       140       150       160
CAACGACTCCAAGATCCTGTCCCTGCAGAACGCTAAGAACACCTGGTCGACACCTTCCGGTTACAACGGCCGA
|||||||| ||||||||||||  |||||||| |  ||||||||||| ||||||  ||| |||| ||||||
CATCAATACCTCCATCCTGAACCTGCGCGTACGACGATCCGATCGACGACCTGTCGTCGGTAACGCTTCCAA
         60        70        80        90       100       110       120

170       180       190       200       210       220       230
GGTCTCCGAGGAGGGTGACGTCCAGGTGACCCCAATCTTCCCATTCGACTTCAAGCTGGGTTCCTGCGGTGA
||||||||| |||||||| |||||||||| |||||  ||||||||| ||||| ||||||||||||||||||
AATCAACACCGTTCGACTTCAAAGTTAACTTGACTTCGATCAAGAACTCTTACATCATCGAAGAAAGACTTCAGCTG------TTCAATCT
130       140       150       160       170       180       190
```

```
2. US-09-910-186A-9 (1-1371)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =  240   Optimized Score =  240   Matches          =  620   Significance = -0.57
Residue Identity =  49%                            Mismatches       =  686   Mismatches   =  593
Gaps             =  111   Conservative Substitutions =                        Gaps         =    0

20        30        40        50        60        70        80
```

3. US-09-910-186A-9 (1-1371)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score   = 240   Optimized Score   = 620   Significance = -0.57
Matches   = 240   Matches   = 686   Mismatches   = 593
Residue Identity = 49%   Conservative Substitutions = 111   Gaps = 0

```
        |  |      ||    |   |   ||    |||    |||  |  |   |||   |  ||   |||       ||
      GGCTGTGTGTAGAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAAT
        1040        1050        1060        1070        1080        1090        1100

      1120        1130        1140        1150        1160        1170        1180
      CAAGGACAACATCATCTTCCAGATCCAGCCAATGAACACACTTACTACTACGCTTCCCAGATCTTCAAGTC
        ||| |     |  ||||    | ||||| |  ||||| | |||| | | | ||  | ||  | |||
      GAAATCCAAGA-------ACGACCAGGGTATCTAACTAACTAACAAATGAATCTGCAGGACAACAATGG
        1110            1120        1130        1140        1150        1160

      1190        1200        1210        1220        1230        1240        1250
      CAACTTCAACGGTGAGAACATCTCCGGTATCTGTTCCATCGGTACCTACAGATTCCGTCTGGGTGGTGACTG
        |||-|-||||  || |||| |  |||     ||    | |    ||   |  | ||||  | | ||||
      TAACGATATCGGT------TTCATCGGTTTCCACCAGTTCAACAATATCGGTAAACTGGTTGCTTCCAACTG
        1170        1180        1190        1200        1210        1220        1230

      1260        1270        1280        1290        1300        1310        1320        1330
      GTACAGACACAACTACTTGGTTCCAACTGTCAAGCAGGGTAACTACGCCTCCTTGCTGGAGTCCACTTCCAC
        |||||  |     | ||  |||  | |  | | ||   |||| | |  ||||| | |||||  | |||| |
      GTACAATCGTCAGATCGAACGTTCCTCCTCGCACTCTGGGTTGCT------CTTG--GGAGTTCATCCCGGT
        1240        1250        1260        1270        1280        1290

      1340        1350        1360        1370
      CCACTGGGGATTCGTCCCAGTCTCCGAGTAA--TAGGAATTC
        |  |||   ||||   |  | |   ||  |   ||||  |
      TGATGACGGTTGGGTGAACGTCCGGCTGTAACCCGGAAAGCTT
        1300        1310        1320        1330    X
```

```
> O <
O| |O   IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-9-inv.res made by bobryen on Thu 7 Nov 102 14:43:14-PST.

Query sequence being compared:US-09-910-186A-9' (1-1371)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-9' (1-1371) with
File :US0812397SA.seq

complement (handwritten)

```
. 100-
     -
     -
   N -
   U 50-
   M -
   B -
   E -
   R -
     -
   O -
   F 10-
     -
   S -
   E 5-
   Q -
   U -
   E -
   N -
   C -           *
   E -
   S -   --------------------------------------------------
     0-      |    |    |    |    |    |    |    |    |    |    |
SCORE 0    6   12   19   25   31   37   44   50   56
STDEV -4  -3   -2   -1    0    1
```

                    PARAMETERS

```
Similarity matrix    Unitary
Mismatch penalty           1
Gap penalty             5.00         K-tuple              4
Gap size penalty        0.33         Joining penalty     30
Cutoff score               1         Window size        500
Randomization group        0
```

              SEARCH STATISTICS

```
              Mean      Median      Standard Deviation
Scores:        45        41              9.24

              CPU                    Total Elapsed
Times:    00:00:00.00                00:00:00.00

Number of residues:              4027
Number of sequences searched:       3
Number of scores above cutoff:      3
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
                                                                Init. Opt.
Sequence Name   Description                    Length Score Score Sig. Frame
--------------  ------------------------------ ------ ----- ----- ---- -----
                **** 1 standard deviation above mean ****
1. US-08-123-975A-6 Sequence 6, Application U  1351    56   435  1.19   0
                **** 0 standard deviation from mean ****
2. US-08-123-975A-4 Sequence 4, Application U  1338    40   404 -0.54   0
3. US-08-123-975A-1 Sequence 1, Application U  1338    40   404 -0.54   0
```

1. US-09-910-186A-9' (1-1371)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

```
Initial Score    =   56   Optimized Score       =  435   Significance  =   1.19
Residue Identity =  418   Matches = 539  Mismatches  =  670
Gaps             =    0   Conservative Substitutions = 104
```

```
            100        110 X     120        130        140        150        160
CCAAGTAGTTGTGTCGTACCAGTCACCACCCAGACGGAATCTGTAGGTACCGATGGAACAGATACCGGAGA
                      ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                      X             10         20         30         40         50

            170        180        190        200        210        220        230
TGTTCTCACCGTGAAGTTGGACTTGAAGATCTGGGAAGCTGGAAGCTGTAGTAAGTGTTGTTCATTGGCTGGATCT
|| |||| || || ||||| ||| || |||||       ||| |||||| ||||| ||| ||||| |||| |||
TG------CGTTACA---AAGACAACAATCTG---ATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGT
                  60             70         80         90        100        110

            240        250        260        270        280        290        300
GGAAGATGATGTTGTCGTTGAACTGAATGACAGACCAGTTCAAACTGACCTCTTCCGGTGAGATGGCTAGTAGTCCTCGGTGGAGT
|||||      ||| ||||| |||||||  |||||| ||||||||||  ||| || |     |||||||
ATACGACGGGTGTTGAACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAA--CTCTAAGATCCGT
              120        130        140        150        160        170        180

            310        320        330        340        350        360        370
GGTTGTCGG---CGTACAGTGGTCGTCCGTTCCTTCCGTTCATGAACAGG---TTGTAGGCCTTGGTTGTTGTTCCTTCTGTGATAGTCATG
||| ||          ||| ||| || |||||| || || |||||       ||| || |||||| ||| || |||   |||
GTTACTTCAGAATCAGAACATCAATCTTCAACTCCGTATTCCTGACTTCTGTCTGGTGCGTTACCTCTGATACGCTTGATGATGATC
              190        200        210        220        230        240        250

            380        390        400        410        420        430        440
TCGAAGTACAGGATGGAACGGTCACCACCTCTGACTCTGGGTGTCGTTGGTGTTACCTCTGATACGCTTGATGATGAAGAAT
||| |||||| || ||| ||| || || || |||||||| |  ||| |||| ||   ||||| || |||||| |||
CCGAAATACAGAAGACGGTATCCAGAATTACATCCACAATGAATACACCATCAACTGACATGAAGAGGAAT
              260        270        280        290        300        310        320

            450        460        470        480        490        500        510
TTGTAACCCTCGTTGAAGTCGTT--GTTGTTA-CGTCTGCGTGTTGAAGACGATCTGTCGGAGTGGCGTAC
|| ||| ||| ||||     |||||   ||| ||   |||||| || || |||| |||||| |||||
CCATCACCAATA-ACCTGAACAATGTAAAATCTACATCACCACGGAAACTGACTCTAATACCGACATCAAA
              330        340        350        360        370        380        390

            520        530        540        550        560        570
ATGTATCGTGTCAAGTAGTCCGATGTGACCATGTAGTACTCCTTG----TTGTATCTCAGG---TCGTTA
||| || |||||  ||  ||  |  |||| ||| |||||    ||||    ||| ||||  |||   |||||
AAATCTGTATTCTTCGAATACAACAT--CCGTGAAGACATCTCTGAAATACATCGCTGGTTCTTCGTTA
              400        410        420        430        440        450        460

            580        590        600        610        620        630        640
CC----CCAGTAGTCCTTGACGACGTTGGTGTACTGCAAGGAGTTGAACAGGATGTTGATGTCCTTACCGTC
||     ||||| || || ||| |||||||| ||| |||||| |||| | ||| ||  ||||| ||| ||||
CCATCACCAAATA-ACCTGAACAATGTAAAATCTACATCACCACGGGAAACTGAATCTAATACCGACATCAAA
              470        480        490        500        510        520        530

            650        660        670        680        690        700        710
CAACTCCTTGGCGAAGATGTAGAAGTCAGGATCCACGATGGTCAGGATCCACATGGTGTTCGGAGTCGGAGTGGATCAGAGCC
||       |||||| ||| || ||||  ||  |  ||||| || ||||||||||| ||| |||||||     ||| ||||||
GACATCCGT---------GAAGTATCGTAACGGTGAAATCATCTTCAAACTGACGGGTGA------
              540        550        560        570        580        590

            720        730        740        750        760        770        780
GGTGTCTGGAGATCTTGTTGATCTCGAAGGTGATGGTCTTGGAGAAGTTGATACCGGTCAACTCCTTGACCTT
```

```
CCTTGGTCTGCTCACGCAGACCGATGGCGGTAG-ATGTCCTCGGTGGAGTG-GTTGTGGGCGTACATGGTCTC
||| ||  | | |   |  |||    |   |||   ||||||||  ||    |  |  |  |  |  |||||| ||
CATCAATACCTCCATCCTGAACCTGCGCTACGATCCAATCACCTGACCTGTTCGCTACGGTTCTCCAA
 60          70          80          90         100         110         120

GTTCTCATGAACAGGTTGTGAGGCCTTGGTCTTGTGATGGTCATGTCGAAGTACAGGATCACCACCCTCTGAC
   340         350         360         370         380         390         400
AATCAACATCGGTTCTAAGTTAACTTCGATCCGATCGACAGAATCAGATCCAGCTGT--------TCAA
 130         140         150         160         170         180

TCTGGGTCGTTGGTGTTACCTCGATACGCTTGATGATGATGCTGTTGAAGTCGTTGTTGTT
   410         420         430         440         450         460         470
GTACAACAGAAATACTA--TATGTTCAATGCTGGTAACAAGAACTCTTACAACAACTCTATGTATACAACTTCTC
 190         200         210         220         230         240         250

ACGTCTGGTGTTGAAGACGATCGTGCTGGAGGTTGGCGTACATGTCAAGTAGTCGATGTTGACCAT
   480         490         500         510         520         530         540
CACCTCCTTCTGGGATCCCGGATCCCGGAAATACTTCAACTCTCTGAACAATGAATACACCATCATCAA
 260         270         280         290         300         310         320         330

GT-------AGTACTCCTTGTTGTATTCAGGTCGTTACCCCAGT-AGTCCTTGACGACGTTGGTGTAC-T
   550         560         570         580         590         600
CTGCATGGGAAACAATTCTGGTTGGAAAGTATCTGAACTACGGTGAAATCTGGACTTGCAGGACAC
 340         350         360         370         380         400

GCAAGGAGTTGAAGGATGGTTGATGTCCTTACCGTCCAACTCCTTGGCGAAGATGTAGAAGTCACGGATCC
   610         620         630         640         650         660         670         680
TCAGGGAAATCAAACAGCGTGTTG--------TATTCAAATACTCTCAGATGATCAACAATCTCTGACTACA
 410                       420         430         440         450         460

ACATGTTGATGTTGTCGGATGGTCGGAGTGATCAGACCGGTGTCTTGGATCTTGTTGATCTCGAAGGTGATGG
   690         700         710         720         730         740         750
TCAATCGCTGGATCTTCGTTGACCATCACCAACAATCGTCTGAAT--------AACTTCCAAAATCTACA
 470                       480         490         500         510         520

TCTTGGAAGTTGATGATGTACCGGTCAACTCCTTCCTTGACCTTGATGGTCGGATCAGCTTGACGGTTGATGTAGATCT
   760         770         780         790         800         810         820
TCAACGGCCGTCGATCGTTGACCAGAAACCGATCTCCAATCTGGTAACTCCACGCCTTC-----TAATAACA
 530         540         550         560         570         580         590

TCATGT-ACCCATCATGTGTTCGGTGACGGTGACACTCAC-CGTACATCTGGATCAAATACTTCAATCTGTTTCGA-
   830         840         850         860         870         880         890
ATGTCGTAGGAGAAGTTGATGGACTGCTCCGGAGTCCGCGTTCGTCTTCAGGGTGACGGAAGTTGTTGGAG
 600         610         620         630         640         650         660

ATGTCGTAGGAGAAGTTGATGGACTGCTCCGGAGTCCGCGTTCGTCTTCAGGGTGACGGAAGTTGGAG
   900         910         920         930         940         950         960
----CAAGAACTGACGAGAAGAAATCAAGACCT-GTACGACAACCAGTCCAATTCTGGTATCCTGAAA
 670         680         690         700         710         720

ATGATACCGGTGGGTGACTACCTGCAGTAGACGTACGACAAAACCTACTACATTGTG---AATCT-GTACGATCCGAACA
   970         980         990        1000        1010        1020        1030
GACTTCTGGGGTGACTACCTGCAGTACACGGTACGCTACGACAAAACCTACTACATTGTG---AATCT-GTACGATCCGAACA
 730         740         750         760         770         780         790

CACTTGTGATTCTGATCCAGAGAGGATGGAGAGGACTCGTACATGGAGTTGTAGACGATGTTCTGTTC
  1040        1050        1060        1070        1080        1090        1100
AATACGTTGA-CGTCAACAATGTAGGTATGGTCTTTGTTACCT-GAAAGGTCCGGCGTGGTTCT-GTTA
 800         810         820         830         840         850         860

TGGGT--GACGATGACCTTACCTCTGTCCTCACCGGAGGAACCCAGCTTGAGTCGAATGGGAAGATTGGG
  1120        1130        1140        1150        1160        1170        1180
 270         280         290         300         310         320         330
```

3. US-09-910-186A-9' (1-1371)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score   =   40   Optimized Score   =   404   Significance = -0.54
Residue Identity   =   40%   Matches   =   485   Mismatches   =   626
Gaps   =   Conservative Substitutions =   91

[DNA sequence alignment data — dense nucleotide sequences with positional numbering (ranging from position 10 through 1371) and alignment match bars, rotated on the page.]

```
> O <
O|O  IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-10.res made by bobryen on Thu 7 Nov 102 14:33:22-PST.

Query sequence being compared:US-09-910-186A-10 (1-450)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-10 (1-450) with:
      File : US08123975A.pep

```
100-

N    -
U 50-
M    -
B    -
E    -
R    -

O    -
F 10-
     -
S 5-
C    -
O    -
R    -
E    -
S  0-
      ----------------------------------------------------
                                            *         *  *
                                            |   |  |   |  |
SCORE  0    14     27     41     55     68     82     96    109    123
STDEV      -5     -4     -3     -2     -1      0      1                1
```

PARAMETERS

Similarity matrix	PAM-150
Threshold level of sim.	168
Mismatch penalty	1
Gap penalty	5.00
Gap size penalty	0.05
Cutoff score	1
Randomization group	0

	K-tuple	1
	Joining penalty	20
	Window size	450

SEARCH STATISTICS

	Mean	Median	Standard Deviation
Scores:	104	89	17.56

	CPU	Total Elapsed
Times:	00:00:00.00	00:00:01.00

Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig. Frame
			**** 1 standard deviation above mean ****		
1. US-08-123-975A-2	Sequence 2, Application U	850	123	251	1.08	0
		**** 0 standard deviation from mean ****		
2. US-08-123-975A-5	Sequence 5, Application U	439	103	238	-0.06	0
3. US-08-123-975A-3	Sequence 3, Application U	415	88	229	-0.91	0

1. US-09-910-186A-10 (1-450)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score	=	123	Optimized Score = 251 Significance = 1.08
Residue Identity	=	25%	Matches = 258 Mismatches = 286
Gaps		28	Conservative Substitutions = 31

```
                  X     10        20        30        40        50
                  MTIPFNIFSYTNNSLLKDIINEYFNNINDSKILSLQNRKNTLVDTSGYNAEV
                  |||  ||  |||||| |  |||||||  || ||||   | ||||||||||
KLYLIGSAEYEKSKVNKYLKTIMPPDLSIYNDTILIEMPNKYNSEILNNIILNLRYKDNNLIDLSGYGAKV
         380         390 X   400       410       420       430       440

                  60        70        80        90       100       110
SEEGDVQLNPIPPFDFKLGSSGEDRGKVIVTQNENIVYNSMYESFSISFWIRINKWVSN------LPGYTII
     |  | |            ||    ||||  ::|| ||  ||||| |||||| |||   |  |||||||
EVYDGVELNDKNQFKLTSSAN---SKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTII
         450       460       470       480       490       500       510

          120       130       140       150       160       170       180       190
DSVKNNSGWSIGIISNFLVFTLKQNEDSEQSINFSYDISNNAPGYNKWFFVTVTNNMGNMKIYINGKLIDT
|||||     ||||   |||| :  ||||| |   ||  : |||   |||| || |   ||||||||||||
NCMKNNSGWKISRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESN
          520       530       540       550       560       570       580

          200       210       220       230       240       250       260
IKVKELTGINFSKTIFEINKIPDTGLITSDSDNIMWIRDFYIFAKELDGKDINILFNSLQYTNVVKDYWG
|||||     ::|| |  |  |          ::|| |||  |        :|||| ||||| ||||||
TDIKDIREVIANGEIIFKLDGDIDRTQF-------IWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWG
          590       600       610       620       630       640

          270       280       290       300       310       320       330
NDLRYNKEYYMVNIDYLNRYMYANSQIVFNTRRNNNDFNEGYKIIIKRIRGNTNDTRVRGGDILYFDMTIN
|  || | | || | || ||| | |  ||   || | |  || ||  ||   |  ||  || | || |||
NPLMYNKEYYMFNAGNKNSYIKLKKDSPVGPILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIV
650       660       670       680       690       700       710       720

          340       350       360       370       380       390
NKAYNLFMKNETM------YADNHSTEDIYAIGLREQTKDINDNIIFQIQPMNNTYYASQIFKSNFNGE
                   || || || |  | |  || || |  | |   | ||| ||| ||||||
RKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTD
730       740       750       760       770       780       790

          400       410       420       430       440       450
NISGICSIGTYRFRLGGDWYRHNYLVPT--VKQGNYASLLESTSTHWGFVPVSE
|  |   | || || ||| | || |||   ||||| ||||||| | ||| ||
EIGLIGHRFYESGIVFEEYKDYFCISKWYLKEVRKPYNLKLGCNWQFIPKDEGWTE
800       810       820       830       840       X 850
```

2. US-09-910-186A-10 (1-450)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score	=	103	Optimized Score = 238 Significance = -0.06
Residue Identity	=	25%	Matches = 115 Mismatches = 274
Gaps		28	Conservative Substitutions = 30

```
                  MTIPFNIFSYTNNSLLKDIINEYFNNINDSKILSLQNRKNTLVDTSGYNAEVSEEGDVQLNPIPPFDFKLGS
                  |||  ||  |||||| |  |||||||  ||
                  FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSA
                  X     10        20        30        40        50
```

```
              260        270        280        290        300        310        320
          360 AIGLREQTKDINDNIIFQIQPMNNTYYASQIFKSNFNGENISGICSIGTYRFRLGGDWYRHNYLVPTVKQG 430
                  :|       |||||||||||||||||||||||||||||||||| :|      :| :
              SALEIPDVGNLSQVVMKSKNDQGITNKCKMNLQDNNGNDIGFHQFNNIAKLVASNWYNRQIERSSRTL
                  330        340        350        360        370        380        390

              440        450
          NYASLLESTSTHWGFVPVSE
              :      ||    |
          GCSWEFIPVDDGWGERPL
              400        410     X
```

```
              80          90          100         110         120         130
          SGEDRGKVIVTQNENIYNSMYESFSISFWIRINKWVSN------LPGYTIIDSVKNNSGWSIGIISNFLVF
           :| ||||  ||::||: ||::||||| :||||||||            :|||||||| ||||| :
          N----SKIRVTQNONIIFNSVFLDFSVSFWIRIPKYKNDGIONYIHNEYTIINCMKNNSGWKISIRGNRIIW
           60          70          80          90          100         110         120

              140         150         160         170         180         190         200         210
          TLKQNEDSEQSINFSYDISNNAPGYNKWFFVTVTNNMGNMKIYINGKLIDTIKVKELTGINFSKTITFEIN
           ||   |: |    | |: |  :|  |||||||||||||  :|||||  |||||||||| ||::
          TLIDINGKTKSVFFEYNIREDISEYINRWFVTITNNLNAKIYINGKLESNTDIKDIREVIANGEIIFKLD
              130         140         150         160         170         180         190

              220         230         240         250         260         270         280
          KIPDTGLITSDSDNINWIRDFYIFAKELDGKDINILFNSLQYTNVVKDYWGNDLRYNKEYYMVNIDYLNRY
              :  |: |  :  | | |  | |  | |    | | | ||:|   :||   |:   |
          GDIDRTQF------IWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSY
              200         210         220         230         240         250

              290         300         310         320         330         340
          MYANSRQIVFNTRRNNNDFNEGYKIIIKRIRGNTNDTRVRGGDILYFDMTINNKAYNLFMKNETM------
            | |  |:|||||||| |||| ||||:||||||||:|||||||||||||||||||| ||:
          IKLKKDSPVGEILTRSKYNQNSKYINYRDLVIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVY
              260         270         280         290         300         310         320

              350         360         370         380         390         400         410
          -YADNHSTEDIYAIGLREQTKDINDNIIFQIQPMNNTYYIASQIFKSNFNGENISGICSIGTYRFRLGGDWY
              |   |:|     |||||||||||||||||||||||||||||||||||||||||||||||||||
          TYKYFKKEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTEIGLIGIHRFYESGIVFEEY
              340         350         360         370         380         390         400

              420         430         440         450
          RHNYLVPT--VKQGNYASLLESTSTHWGFVPVSE
              :    :  :|:   ||    |
          KDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
              410         420         430     X
```

3. US-09-910-186A-10 (1-450)　Sequence 3, Application US/08123975A
   US-08-123-975A-3

```
Initial Score        =   88   Optimized Score    =  229   Significance =  -0.91
Residue Identity     =  27%   Matches            =  117   Mismatches   =   251
Gaps                 =   32   Conservative Substitutions =  30
```

```
              20          30    X     40          50          60          70          80
          LKDIINEIFNNINDSKIILSLQNRKNTLVDTSGYNAEVSEEGDVQLNPIFPPDFKLGSSGEDRGKVIVTQNEN
           |:           ||  ||:    |                       ||    ||:::|:||:|
          RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQL--FNLESSKIEVILKNA
              X         10          20          30          40          50

              90          100         110         120         130         140         150
          IVYNSMYESFSISFWIRINKWVSNLP---GYTIIDSVKNNSGWSIGIISNFLVFTILKQNEDSEQSINFSYDI
          ||||||||||||||||||||||||      |||||||||||||||||||| : :::|:|  : ::|:
          IVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQ
              60          70          80          90          100         110         120

              160         170         180         190         200         210         220
          SNNAPGY-NKWFFVTVTNNMMGNMKIYINGKLIDTIKVKELTGINFSKTITFEINKIPDTGLITSDSDNINM
              |    | || |||:|||:|||||||| |  :  |||||  : |:::  |
          MINISDYINRWIFVTITNNRLNNSKIIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDT------HRYI
              130         140         150         160         170         180

              230         240         250         260         270         280         290
          WIRDFYIFAKELDGKDINLLFNSLQYTNVVKDYWGNDLRYNKEYYMVNIDYLNRYMYANSRQI------
           |||||||||||||  :|::|||| | ||   :|| |  :||||||||||||||||||:::| :
          WIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGP
              190         200         210         220         230         240         250

              300         310         320         330         340         350
          ---VFNTRRNNNDFNEGYKIIIKRIRGNTNDTRVRGGDILYFDMTINNKAYNLFMKNETMYADNHSTEDIY
                    | |  ||||||||:||||||||:|||||||||  |:   || |  ||::   |:
          RGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNIVRNDRVYINVVKNKEYRL----ATNASQAGVEKIL
              260         270         280         290         300         310
```

```
> O V
O| |O   IntelliGenetics
> O V

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-11.res made by bobryen on Thu 7 Nov 102 14:43:36-PST.

Query sequence being compared:US-09-910-186A-11 (1-1374)
Number of sequences searched:        3
Number of scores above cutoff:       3

Results of the initial comparison of US-09-910-186a-11 (1-1374) with
    File : US08123975A.seq
```

```
1. US-09-910-186A-11 (1-1374)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score   =   454     Optimized Score        =   624     Significance    =   0.59
Residue Identity =  508     Matches                =   508     Mismatches       =   619
Gaps             =   49     Conservative Substitutions =   669  Conservative Substitutions =   0
```

```
                60        70       X  80        90       100       110       120
CCATTCAACATCTTCTCCTACCACCAACAACTCCTTGT-TGAAGGACATCATCAACGAGTACTTCAACTCCAT
                ||||| | ||  |||||| ||  ||||||||||||||||||||| |||||| |||
         CTCGGACCCATGGCGTCGTCGTCGTCCTTCACTGAATACATCAAGAACAT
                 X        10        20        30        40        50

              130       140       150       160       170       180       190
CAACGACTCCAAGATCTTGTCCTTGCGAACAAGAAGAACGCCCTTGGTCGACACCTCCGGTTACAACCCCGA
         |||| ||| |||| | |||| ||||||||||||  ||| |||| |||||| ||| |||
CATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCCGTCTCGCTACGCGTTCCAA
         60        70        80        90       100       110       120

              200       210       220       230       240       250       260
GGTCGAGTCGGTGACAAGTCCAGTTGAACACCATCTACACCAACGACTTCAAGTTGTCCTCTTCCG---G
         || | |||||||  ||| ||| || |||| |||||| |  || | || |||||||||
AATCAACACCGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATC
         130       140       150       160       170       180       190

              270       280       290       300       310       320       330
TGACAAGATCGTCAACTTGAACAACAACATCTTGTACTCCGGCCATCTACGAGAACTCCTCGTCTCCCTT
         | ||| | || |||| |||||| ||| ||||||| |||| | ||||||| |||||| |||
TTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATCGTATACGAAAAACTTCTCCACCTCCTT
         200       210       220       230       240       250       260

              340       350       360       370       380       390       400
CTGGATCAAGATCTCCAAGGACTGA---CCAACTCCC---ACAACGGTACACATCATCAACTCAACTCATCGA
         |||| | |  |||  |||  ||| | ||||  ||||||||| ||||||| |||||||||
CTGGATCCGTATCCCGAAATACTTCAACTCTCGAACCATCCATCTGAACAATGAATAACACCATCATCAACTCAACTGCATGGA
         270       280       290       300       310       320       330       340

              410       420       430       440       450       460       470
GCAGAACTCCCGGTTGGAAGTTGTGTATCCGTAACGGTAACATCCAGTGGATCTTGCAGGACGTCAACCGTAA
         ||||||| |  || ||| | || |||  |||  || | |||| ||||||| ||| |||
AAACAATTCTGGTTGGAAGTATCTGAACTACGGTGAAATCATCTGAACTCGTGAAATCATCTGGACTCGCAGGACACTCAGGAAAT
         350       360       370       380       390       400       410

              480       490       500       510       520       530       540
GTACAAGTCCTTGATCTTCGACTACTCCGAGTCCTTGCTCCCACACCGGTTACACCAACAAGTGGTCTTCTCGT
         || |  |||||||||| || || |||| ||| | |||||| |||||||| ||| ||||||
CAAACAGCGTGTTGTTGTTATTCAAAATACTTCCAGATGATCAACATCACATCTCCAGCTACACTCAACTCGTGGATCTTCGT
         420       430       440       450       460       470       480

              550       560       570       580       590       600       610       620
CACCATCACCAACAACATCATGGGTTACATGAAGTTGTACATCAACCGTGAGTTGAAGCAGTGCCAGAAGAT
         |||||||||||| ||  |||   ||||||||||||||  |||||||   ||| | |||||
TACCATCACCAACATCGTCTGAATAACTCCAAAATCTACAAACATCTAATAACATCATGTTCAAACTGGATCTTCAAACTGGACACCG
         490       500       510       520       530       540       550

              630       640       650       660       670       680       690
CGAGGACCTGCAGGAGGTCAAGCTGGACAAGACCATCGTCTTCGGTAATCGACGAGACAATCGACGAGAACCA
         | ||||  | ||| || | ||| ||||||| ||||||||||| ||| |||| ||||||||||
CTCCAATCTGGGTAACATCCAGCGTCTAATAACATCATGTTCGTTGTCGTTGACACTCACCG
         560       570       580       590       600       610       620

              700       710       720       730       740       750       760
GATGTTGTGGATTCGTGACTTCAACATCTTCTCCAAGGAGGTGTTCCAACGAGGACAATCAACATCGTCTACGA
         | |||||  | ||| || ||| ||||| || |  ||||| | |  ||||| |||
         700       710       720       730       740       750       760
```

```
                         50    101    151    202    252    303    353   404    454
SCORE 0    50         101    151    202    252    303    353   404    454
STDEV     -9    -8    -7    -6    -5    -4    -3    -2    -1    0

                                                    PARAMETERS

Similarity matrix    Unitary        K-tuple              4
Mismatch penalty     1              Joining penalty      30
Gap penalty          5.00           Window size          500
Gap size penalty     0.33
Cutoff score         1
Randomization group  0

                                              SEARCH STATISTICS

Scores:         Mean        Median          Standard Deviation
                431         387             39.26

Times:          CPU                         Total Elapsed
                00:00:00.00                 00:00:00.00

Number of residues:              4027
Number of sequences searched:       3
Number of scores above cutoff:      3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

2. US-09-910-186A-11 (1-1374),
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score = 454   Optimized Score = 624   Significance = 0.59
Residue Identity = 50%   Matches = 669   Mismatches = 619
Gaps = 49   Conservative Substitutions = 0

```
260
ACAAGAACGACGTATCGCAGAATTACATCCACAATGAATACACCACCATCATCACTCACTCTGCTGGAGAATAACTCTG
  ||                   |||||||||||||| |||||||| |||| |||||||||||||||||| |||||
          270       280       290       300       310       320       330

420
GTTGGAAGTTGTGTATCC---GTAACGGTAACATCGAGTGGATCTTGCAGGACGTGCAAGCGTAAGGTACACAGT
||||||||||  |||| |     |||||||||||||||||||||| |
          430       440       450       460       470       480
GTTGGAAGATCCATCCGCGGTAACCGTAATCATC---TGGACTCGATGCATATCAACGGTAAGACCCAAAT
          340       350       360       370       380       390       400

490
CCTTGACTTCGACTACTCCGAGTCCTTGTCCCACACCGGTTACACCAACAAGTGGTTCTTCGTCTCACCATCA
|| |||||||||||  |||||  ||||||||||||||||||||||||| |||||| |||||||||||||||||
          500       510       520       530       540       550
CTGTATTCTTCGGATACACAACATCCTGAAGACATCTCAATACATCAATGCGCTGTGTTCTTCGTTCGTTACCATCA
          410       420       430       440       450       460       470
```

(Additional sequence alignment blocks continue)

```
3.  US-09-910-186A-11 (1-1374)
    US-0B-123-975A-6 Sequence 6, Application US/08123975A

    Initial Score    =   386   Optimized Score   =   621   Significance   = -1.15
    Residue Identity =   51%   Matches           =   557
    Gaps             =         Mismatches        =       0
                               Conservative Substitutions = 104
```

```
80        90 X     100       110       120       130       140
ACACCAACAACTCCTTGTTGAAGGACATCAACGAGTACTTCAACTCCATCAACGACTCCAAGATCTTGT
                    |||||      ||||   |||||||||||  |||||||||    ||| |||
ATGGGCTTCAACAAATACAATTCCGAAATCCTGAACAA---TATCATCCTGA
   X           10        20        30        40
```

```
CTTGCCAGCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTCT
1110      1120      1130      1140      1150      1160      1170      1180

1240      1250      1260      1270      1280      1290      1300
AAGCCCTGGCGTTCTCCTTCAAGAACGCCTACACTCCTGTCGCCGTCAACTACGAGACCAAG------
 |-|-|--|-|--| ||||| -|-|-|||-||-|||||-|--| --||||||-| |  |||
ACGAATCTGGTATCGTATTCGTAGAAGAATACAAAGACTACT-TCTGCATCTCCAAATGGTACCTGAAGGAAGTT
      1190      1200      1210      1220      1230      1240      1250

      1310                1320      1330      1340      1350      1360
-----CTGCTGTCCACC-------TCCTCCTTCTGGAAGTTCATCTCCCGTGACCCAGGTTGGGTCGAG
     |-||-|| ||      |-|| ||||||| -| |||||||  |-|||||| |||
AAACGCAAACCGTACAAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAA
      1260      1270      1280      1290      1300      1310      1320

      1370  x
TAATAGGAATTC
|| || |
TAGTAACCTCTAGAGTCGAGGCCTGCAG
      1330  X 1340      1350
```

```
> O V    IntelliGenetics
O| |O
> O V

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-11-inv.res made by bobryen on Thu 7 Nov 102 14:44:07-PST.

Query sequence being compared:US-09-910-186A-11' (1-1374)
Number of sequences searched:     3
Number of scores above cutoff:    3

Results of the initial comparison of US-09-910-186a-11' (1-1374) with:
    File "US08123975A.seq"
```

(handwritten annotation: complement)

```
100-
    -
    -
    -
N   -
U 50-
M   -
B   -
E   -
R   -
    -
O   -
F 10-
    -
S   -
E  5-
Q   -
U   -
E   -
N   -
C   -
E  0- ------|------|------|------|------|------|------|------|------|------|------
S     |    |    |    |    |    |    |    |    |    |    |    |
      -5  -4  -3  -2  -1   0   1  *                    *          *  |  |
SCORE 0  10  15  20  26  31  36  41  46
STDEV -6  -5  -4  -3  -2  -1   0   1
```

```
PARAMETERS
Similarity matrix   Unitary        K-tuple           4
Mismatch penalty    1              Joining penalty   30
Gap penalty         5.00           Window size       500
Gap size penalty    0.33
Cutoff score        1
Randomization group 0

SEARCH STATISTICS
Scores:    Mean    Median    Standard Deviation
           42      37        5.77

Times:     CPU            Total Elapsed
           00:00:00.00    00:00:00.00

Number of residues:            4027
Number of sequences searched:  3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                     Init.  Opt.
Sequence Name    Description                 Length  Score  Score  Sig.   Frame
---------------------------------------------------------------------------------
1. US-08-123-975A-4  Sequence 4, Application U  1338   46    308   0.69    0
2. US-08-123-975A-1  Sequence 1, Application U  1338   46    308   0.69    0
               **** 1 standard deviation below mean ****
3. US-08-123-975A-6  Sequence 6, Application U  1351   36    296  -1.04    0
```

```
1. US-09-910-186A-11' (1-1374)
   US-08-123-975A-4  Sequence 4, Application US/08123975A

Initial Score    =  46    Optimized Score         =  308   Significance  =  0.69
Residue Identity =  41%   Matches                 =  366   Mismatches    =  437
Gaps             =  3     Conservative Substitutions = 71                 =  0
```

```
             520        530        540        550        560        570        580
GTAACGGTCGATGTAGTTGTCGTTGATGATGTAGTACTCGGTCGAACTTCAGTGGGTTACCCAGTAGTC
                           |||  | ||||  |  ||||  ||||| |
                CTCGAGCCATGGGCTCGTCTGCTGTCTTCACTTGAATACATCAAGAACAT
                  X           10        20        30        40        50

             590        600        610        620        630        640        650
CTTGATGACGTTCCTCAGAGTCGACCCTCGTAGACGATGTTGATGTCCTCGTTGGACAGCTCCTTGGAGAA
 | ||| ||||         | ||||  |         ||| |||||     ||||
-CATCAATACCTCCATC-----CTGAACCTGCGCTACGAATCCAATCACCTGATCG--ACCTGTCTCGCTAC
      60                70        80        90       100       110

             660        670        680        690        700        710        720
GATGTTGAAGTCACGAATCCACACATCGGTTCTCGTCGTTCGATGTTCGATGAACCGAAGACGATGGTCTT
 |  |          |||  | ||||||   ||   | |||   ||||||||  |  ||||
GCT------TCCAAAATCAACATC----GGTTCT-----AAAGTTAACTTCGATCCGATCGACAAGAATCAG
      120       130       140       150       160       170

             730        740        750        760        770        780        790
GTCCAGCTTGACCTCGTCCAGGTCCTCGATCTTCTGGGACTGCTTCAACTCACCGTTGACATGTACAACTTCAT
|||||||  |   ||| ||  |  |    |||| | |||  |||  |||||  |||||||  |||| |||||
ATCCAGCTGTTCAATCTGGA-ATCTTCCAAAATCGAAGTTAATCCTGAGAGAATGCTATCGTATACAACTCTAT
      180       190       200       210       220       230       240

             800        810        820        830        840        850
GTA------ACCCATGATGTTGTTGGATCCGAGAA------GAACCACTTGTTGGTGTAACCGGT
|||         |  | |  ||||| ||  | |||           |||||  || ||  || |||
GTACAGAAAACTTCTCCACCTCCTTCTCGATCCGGATAAC-----GAACCACTTCAACTCCATCTCCTGACAATGA
      250       260       270       280       290       300       310

             860        870        880        890        900        910        920
GTGGGACAAGGACTCGGAGTAGTCGAAGATCAAGGACTTGTACTTACCGTTGACGTCCTCGCAAGGATCCACTC
|   |  ||  ||| ||  |||| || |  ||| |   | |||  ||| ||| |||| || |||  |||   |||
ATACACCATCATCAACTCAACTGCATGGAAAACAATTCTGGTTGGAAGTATCTCGAACTACGGTGAAATCATCTG
      320       330       340       350       360       370       380

             930        940        950        960        970        980        990
GATGTTACCGTTACGGATACACAACTTCAACCGGAGTTCTCGTCGATGGAGTTGATGGATGTGTACTCGTT
||||||||  | | |  |||| ||  ||||  | ||  | | || || | |  | |||||  | | || |||
GACTCTGCAG---GACACTTCAGGAAGAAATCAAACACGCGTGTGTATTCAAATACTTCTCAGATGATCAAC--AT
      390       400       410       420       430       440       450

            1000       1010       1020       1030       1040       1050       1060       1070
GTGGGAGTTGGTCAAGTCCTTGGAGATCTTGATCAGGAGGAGGACAGGAGGAGTTCTCGTAGATGGGGGAGTA
||||||| |  |  |||  |  || || |||| | ||  ||||  || |  ||   ||| |  || | |  ||||
CTCTGACTACATCAATCGTCGGATCTTCGTTGTTACCATCACCAACAATCCGCTCTGAATAACTTCAAAAATCTACAT
      460       470       480       490       500       510       520

            1080       1090       1100       1110       1120       1130       1140
CAAGAGTGTTGTGTTCAAGTTGACGATGAGCCATGAATGATCTTGTCACCGGAAGAGGAGCAACTTGAAGTCGTTGGTGTAGAT
|| || ||   ||| |  |  ||||| |||       | ||| |||| ||| |  |||||||  ||||  |||  || ||  |||||
CAACGGCGCCGTCGATCGACCAGAACCGATCT-----CCAATCTGGGTAACATCCACGCTTCTAAATAACAT
      530       540       550                  560       570       580       590

            1150       1160       1170       1180       1190       1200       1210
GGTGTTC-AACTGACGGTTGTCACCGACTTCACCGACTTCGGCGTTGTAACCGGAGGTGTCGACCAAGGCGTTCT
|||||||||  |  | ||  |||
```

```
2.  US-09-910-186A-11' (1-1374)
    US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =   46    Optimized Score  =  308    Significance  =  0.69
Residue Identity =   41%   Matches          =  437    Mismatches    =  437
Gaps             =         Conservative Substitutions =  71
```

```
3.  US-09-910-186A-11' (1-1374)
    US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =   36    Optimized Score  =  296    Significance  =  -1.04
Residue Identity =   40%   Matches          =  349    Mismatches    =  468
Gaps             =         Conservative Substitutions =  44
```

```
     AGTCGAAGAGATCAAGGACTTGTACTTACGGTTGACG--TCCTGCAAGATCCACTCGATGTTACCGTTACGGAT
       | ||||||           | |      ||||  |   |  || | | || ||||  | |||||||  |  | |||
     GTTGGAAGATC------TCCATCCGCGTAACCGTATCATCCGGACTCTGGACTTCGATCGAATATCAACGGTAAGACC
         340              350              360              370           380              390

     950              960              970            980          990            1000           1010
     ACACAACTTCCAACCGGAGTTCTGCTCGATGGAGTTGATGATGGTGTACTCGTTGTCGGGAGTTGGTTCAAGTC
       | ||||||| |  ||  ||   | ||     |  |||  |   |    ||    |  |  | | ||   ||| |
     AAATCTGTATTCTTGAAATACAACATCCGTGAAG-ACATCTCTGAATACATCAATCGCTGGTTCTTCGTTAC
         400            410            420            430            440            450            460

     1020            1030           1040            1050           1060            1070            1080
     CTTGGAGATCTTGATCCAGGAGGAGCACAGGAGTTCTCGTAGATGGCGGAGTACAAGAGATGTTGTTGTTCAA
       |   ||| | |      |  | |   |     | || ||    ||  | |  |   | |    |||    |   | |
     CATCACCAATAACCTGAACATGCTAAAATCTACAATCAACGGGTAAACTGGAATCTA--ATACCGACATCAAA
         470            480            490            500            510            520            530

     1090            1100            1110            1120            1130            1140            1150
     GTTGACGATGATCTTGTCAC--CGGAAGAGGACAACTTGAAGTCGTTGGTGTAGATGCGTTCAACTGGACG
       | ||| ||   |  |  ||   ||  |  | |    | ||  |||   |     | |     |  |||  ||
     GACATCCGTGAAGTTATCGGTAACGGTGAAATCATCTTCAAACTGGACGGGTGACATCGATCGTACCCAGTTC
         540            550            560            570            580            590            600

     1160            1170            1180            1190            1200            1210            1220
     TTGTCACCGACTCTGACCTCGGCGTTGTAACCGGAGGTGTC---GACCAAGGCGTTCTTCTTGTTCTGCAAG
       |||     | | |      |||   | || |  |      |    || ||        |    | | | || |
     ATCTGGATGAAATACTTCTCCATCTTCACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATC
         610            620            630            640            650            660            670

     1230            1240            1250            1260            1270            1280            1290
     GACAAGAGATCTTGGAGTCGGTTGATGGAGTTGAAGTACTCCGTTCGTTGATGATGTCCTTCAACAAGGAGT---TGTTG
       | ||  | |  |      |  | | ||  |||||    | | |||  |      | |  |     |  | || |      ||||
     CAGTCTTACTCCGAATAACCTGAAAGACTTCTGGGGTAATCCGCTGATGGTAACAACAAGAAATACTATATGTTC
         690            700            710            720            730            740            750

     1300            1310            1320            1330            1340            1350
     GTGTAGGAGAAGAATGTTGAATGGCCATGGTGTTCTCGAAGGACTC----GTTGACCTTAGCC-------TTC
       |   |  |   |   | |  || ||      ||||    | | ||||     ||  || |  |  |  |  | |||
     AATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAGACTCTCCCGTTGGTGAAATCCTGACTCGTTCC
         760            770            780            790            800            810            820

     1360            1370        X
     AAACGGCATCGTGAATTC
       |||  |  ||| || |  |  ||
     AAATACAACCAGAACTCTAAATACATCAACTACCGCG
         830            840 X            850            860
```

```
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-12.res made by bobryen on Thu 7 Nov 102 14:33:46-PST.

Query sequence being compared:US-09-910-186A-12 (1-451)
Number of sequences searched:               3
Number of scores above cutoff:              3

   Results of the initial comparison of US-09-910-186A-12 (1-451) with:
     File : US08123975A.pep
```

```
100-
    -
N   -
U 50-
M   -
B   -
E   -
R   -
    -
O   -
F 10-
    -
S   -
E  5-
Q   -
U   -
E   -
N   -
C   -
E   -                                              *
S  0----------------------------------------------------------
       ||   ||   ||   ||   ||   ||   ||   ||   ||  ||  ||
SCORE 0 20   39   59   98  118  138  157  177
STDEV -4  -3   -2   -1    0    1    1
```

```
                    PARAMETERS

Similarity matrix    PAM-150      K-tuple                1
Threshold level of sim.  16%
Mismatch penalty     1            Joining penalty       20
Gap penalty          5.00         Window size          451
Gap size penalty     0.05
Cutoff score         0
Randomization group  0

                 SEARCH STATISTICS

Scores:          Mean      Median      Standard Deviation
                 147       120              29.05

Times:           CPU                    Total Elapsed
          00:00:00.00                  00:00:00.00

Number of residues:            1704
Number of sequences searched:     3
Number of scores above cutoff:    3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence was not found.

The list of best scores is:
```

```
Sequence Name    Description                                      Length  Init.  Opt.   Sig. Frame
                                                                          Score  Score
                 **** 1 standard deviation above mean ****
                 ****   0 standard deviation from mean ****
1. US-08-123-975A-3 Sequence 3, Application U   415    177    236    1.03    0
2. US-08-123-975A-2 Sequence 2, Application U   850    145    265   -0.07    0
3. US-08-123-975A-5 Sequence 5, Application U   439    119    244   -0.96    0
```

```
1. US-09-910-186A-12 (1-451)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =   177   Optimized Score  =   236   Significance =    1.03
Residue Identity  =   26%   Matches          =   109   Mismatches   =     267
Gaps              =     8   Conservative Substitutions =              28
```

```
           30        40        50        60        70        80        90
LKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRVGDNVQLNTIYTNDFKL-SSSGDKIIVNLNNNIL
             |:||:|||:.::|:|    .: |||||||.:|:||  |||:||||||||||
           RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
X                    10        20        30        40        50

          100       110       120       130       140       150       160
YSAIYENSSVSFWIKISK--DLTNSHNEYTIINSIEQNSGWKLCIRNGNIEWILQDVNRKYKSLIFDYSESL
|:|||::||:|||||:||:| |||||  |   |||||  |   ||||| ||::| || :|
YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIWTLQDTQEIKQRVVFKYSQMI
            60        70        80        90       100       110       120

          170       180       190       200       210       220       230       240
SHIGYTNKWFFVTITNNIMGYMKLYINGELKQSQKIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSK
  |:|:||||||||||| |||  |:|||||.: | :|:|  |:: |:: | :| | | :| :|:|||
NISDYINRWIFVTITNNRLNNSKIYINGRLIIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
           140       150       160       170       180       190

          250       260       270       280       290       300       310
ELSNEDINIVEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYIAPESNVLVLVQYPDLSKLYTGNPITI
||:| :|| :::||::|:.::|:|::|  :|    |:||  ||:|
ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTNIY
200       210       220       230       240       250       260

          320       330       340       350       360       370
KSVSDKNPYSRILN----GDNIILHMLYNSRKYMIIRDTDTIYATQGGECSQNCVYALKLQSNLGNYCIGI
            :::.        |:|| |  ||:|        ||| ||      ||||  ||
LNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
270       280       290       300       310       320       330       340

          380       390       400       410       420       430
FSIKNIVSKNKYCSQIFSSFRENTMLLADIIKPWRFSFKNAYTPVAVTNYETKLLSTSSFWKFISRDPGWVE
             |:|| ::|  |:||||||:|| | :| |||: || :|  |||  | :|| |::| |||:
VMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGE
350       360       370       380       390       400       410       X

RPL
```

```
2. US-09-910-186A-12 (1-451)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score     =   145   Optimized Score  =   265   Significance =   -0.07
Residue Identity  =   30%   Matches          =   147   Mismatches   =     273
Gaps              =    31   Conservative Substitutions =              25
```

```
          X         10        20        30        40        50
MRLKAKVNESPENTMPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKN
          :|||| |:|:||  :| ||| |:|: |  :||||||||||||||||||
LKKNLLNYIDENKLYLLIGSABYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDN
370       380       390       400       410       420       430

          60        70        80        90       100       110       120
ALVDTSGYNAEVRVGDNVQLNTIYTNDFKLSSSGDKIIVLNNNILYSAIYENSSVSFWIKISKDLTNS---
```

```
TDIYATQGGECSQNCVYALKLQSNLGNYGIGIFSIKNIVSKNKYCSQIFSSFRENTMLLADIYKPWRPSFK
EKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDESTDEIGLIGIHRFYESGIVFEE---YKDYFC
340        350        360        370        380        390        400
420        430        440        450
NAYTPVAVTNYETKLLSTSSFWKFISRDPGWVE
       |   |  |||  :||:|   |||||
ISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
410        420        430          X
```

```
|:|||||||||||  ||||| |||  |  |||||    ||||||:|
NLIDLSGYGAKVEVYDGVELNDKNQFKLT-SSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN
440        450        460        470        480        490        500
--HNEYTIINSIEQNSGWKLCIRNGNIEWIILQDVNRKYKSLIFDYSESLSHTGYTNKWFFVTITNNIMGYMK
 ||||||||||||  ||||||||| |||||:|||| |||||||||||||:||:||||||||||||| :||||
YIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN-LNNAK
510        520        530        540        550        560        570
LYINGELKQSQKIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKELSNEDINIVYEGQILRNVIKDY
||||: ||||||||| |||||||||| |||| :| ||:|||||||||||||||||||  ||||| |||||||
IYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDF
580        590        600        610        620        630        640
WGNPLKFDTEYYIINDNYIDRYIAPESNVLV--------LVQYPDLSKLYTGNPITIKSVSDKNPYSRI
||||: ||| || |||  |||||||||||||          ||:|||||||||||||||||||| |||
WGNPLMYNKEYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLIIGEKFIIRRKSNSQSINDD
650        660        670        680        690        700        710
LNGDNIILHMLY--------NSRKYMIIRDTDTIYATQGGECSQNCVYALKLQSNLGNYGIGIFSIKNIVS
        :                |||||       |  |  |  ||||||||||||||||||||||||||
IVRKEDYIYLDFFNLNQEWRVYTYKYFKKKEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEES
720        730        740        750        760        770        780        790
                                   X
390        400        410        420        430        440
KNKYCSQIFSSFRENTMLLADIYKPWRPSFKNAYTPVAVTNYETKLLSTSSFWKFISRDPGWVE
       |   |     ||||| |||||||  |||| |||  :||:|   ||:||  ||||||
TDEIGLIGIHRFYESGIVFEE---YKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
800        810        820        830        840        850
```

3. US-09-910-186A-12 (1-451)
   US-08-123-975A-5 sequence 5, Application US/08123975A

Initial Score   = 119   Optimized Score =   244   Significance = -0.96
Residue Identity = 30%   Matches   =   255   Mismatches   = 136
Gaps   = 31   Conservative Substitutions = 23

```
ENTMPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRVGDNVQLNFIYTNDFKLS
                                                      |
                                    FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLT-S
                                      X                    10        20        30        40        50
20   X   30 X   40        50        60        70        80
SSGDKIIVNLNNNILYSAIYENSVSFWIKISKDLTNS----HNEYTIINSIEQNSGWKLCIRNGNIEWIL
|: ||:|||       ||::||:  ||  ||||||           |||||||||||  |||||||| ||||||
SANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTL
60        70        80        90        100        110        120
90        100        110        120        130        140        150
QDVNRKYKSLIFDYSESLSHTGYTNKWFFVTITNNIMGYMKLYINGELKQSQKIEDLDEVKLDKTIVFGIDE
|:||:|  :||||||||||||||||||||:|| |||||||:|| ||||| :|||||||||||||:|:|
IDINGKTKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG
130        140        150        160        170        180        190
160        170        180        190        200        210        220
NIDENQMLWIRDFNIFSKELSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYIAPESNVLV
   |||:|||||||||||||||||||  ||| |||||:|| |||||: ||| || |||  |||||||||||||
DIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYMFNAGNKNSYIKLKKDSPV
200        210        220        230        240        250        260
230        240        250        260        270        280        290
--------LVQYPDLSKLYTGNPITIKSVSDKNPYSRILNGDNIILHMLY--------NSRKYMIIRD
          ||:|||||||||||||||||||| |||   :        |           ||||||
GEILTRSKYNQNSKYINYRDLIIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEE
270        280        290        300        310        320        330
300        310        320        330        340
350        360        370        380        390        400        410
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-13.res made by bobryen on Thu 7 Nov 102 14:44:27-PST.

Query sequence being compared:US-09-910-186A-13 (1-1400)
Number of sequences searched:          3
Number of scores above cutoff:         3

Results of the initial comparison of US-09-910-186A-13 (1-1400) with:
       File : US08123975A.seq
```

```
100-

 N -
 U -
50- M -
 B -
 E -
 R -

 O -
10- F -

 S -
 5- E -
   Q -
   U -
   E -
   N -
   C -
   E -                                                          *
 0-S -
   -------------------------------------------------------------------
SCORE 0   47    95   142   190   237   285   332   380   427
STDEV     -5    -4    -3    -3    -2    -2    -1     0
```

```
              PARAMETERS

Similarity matrix      Unitary
Mismatch penalty       1        K-tuple              4
Gap penalty            5.00     Joining penalty      30
Gap size penalty       0.33     Window size          500
Cutoff score           1
Randomization group    0
```

```
              SEARCH STATISTICS

Scores:     Mean      Median      Standard Deviation
            392       323         60.62

Times:      CPU                   Total Elapsed
            00:00:00.00           00:00:00.00

Number of residues:             4027
Number of sequences searched:   3
Number of scores above cutoff:  3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                                          Init.  Opt.
Sequence Name    Description                                     Length  Score  Score  Sig.  Frame
----------------------------------------------------------------------------------------------------
1. US-08-123-975A-4   Sequence 4, Application U       1338   427   692   0.58   0
2. US-08-123-975A-1   Sequence 1, Application U       1338   427   692   0.58   0
                **** 1 standard deviation below mean ****
3. US-08-123-975A-6   Sequence 6, Application U       1351   322   612  -1.15   0


1. US-09-910-186A-13 (1-1400)
   US-08-123-975A-4  Sequence 4, Application US/08123975A

Initial Score      =    427   Optimized Score       =   692   Significance =   0.58
Residue Identity   =    54%   Matches               =   739   Mismatches   =   539
Gaps               =     0    Conservative Substitutions =  72
```

```
         70         80         90        100        110        120        130        140
TCCTTTTAAGCTTCTTCTTCTATACAGATGATAAAATTTAATTTCCTACTTCAACAAGTTCTTCAAGAGAAT
                      CTCGAGGCCATGGCTCGGTCGTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                       X      10         20         30         40         50

        150        160        170        180        190        200        210
TAAGCTCTTCCGTTTAAAACATGAGATACAAGAATGATAAATACGTCGACACTTCCGGTTACGACTCCAA
 | ||| |||||||  |  |  | | ||  ||||  || | |||||||  ||||| |||  |||||| ||||
CATCAATAACCTCCATCCTGAACCTGCGCTACGACCTGTCTCGCTACGCTACGCTACCGTCGCTACGTTCCAA
         60         70         80         90        100        110        120

        220        230        240        250        260        270        280
TATCAACATTAACGGTGACGTGTACAAGTGACTACCCAATTAACAAAAACAATTCGGTATCTACAACGACAAGCT
|||||||    |     ||  | | |  | ||  ||||  |||||||||||||  ||||| |||| || ||||||
AATCAACAACTCGGTTCTCAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATC
        130        140        150        160        170        180        190

        290        300        310        320        330        340        350
TTCCGAGGTCAACATCTCTCAAAACGACTACATTATCTACGACAACAAGCATCTCATGTACGAAAACTTCTCCAATTCTTT
|||||| |     ||      |||  |  | | | ||   | | ||  |  || |||  | ||||| || || |||
TTCCAAAATCGAGTTATCCTGAAGAATGCATCGTATACAACTCTATGTACGATACGACTCTCCACCTCCTT
        200        210        220        230        240        250        260

        360        370        380        390        400        410        420
CTGGGTCAGGATTCCTAACTACGACAACAAGAATCGTCAACGTAACAACGATACGGTAACTANTCAACTCAACTGTAT
|| |    | |  | ||||||  ||  ||   |||| |   | ||||| |  |||  |||| || || |||||| |||||
CTGGATCCGTATCCGAAATAGTTCAAC---TCCATCTCTGAACAATGAATCACCATCATCAACAATCAACTGCCAT
270        280        290        300        310        320        330

430        440        450        460        470        480        490        500
GAGAGACAACACCCGGGTGGAAGGTCTCTCTAACCACAACGAGATCATTGGACCTTGGACCTTGCAAGACACGGC
|  || |  |||| || ||| |  ||||| | ||| || | | |  ||||| |||  |||||| || |  ||||
G---GAAAACAATTCTGGTTGGAAAGTATCTCGAAGTACGGTGAAATCATCTGGACTCTGCAGGACACTCA
340        350        360        370        380        390        400

        510        520        530        540        550        560        570
AGGTATTAACCAAAAGTTAGCATTCAACTACGTAACGCAACGGTATTCTTGACTACATCAACAAGTGGAT
|| ||||  ||     ||| ||   ||||  ||  || | ||||  |||||||||| |  || ||| ||||
GGAAATCAAACAGCCGTGTTGTATTCAAATCAAATACTCTCGACGATGACTCAACAATCGCCTGGAT
410        420        430        440        450        460        470

        580        590        600        610        620        630        640
TTTCGTCACTATCACTAACGACAGATTAGGTGACTCTAAGCTTACATTAACGGTAACTTAATCGACCAAAAA
|| |  |||||||| |||| || ||| |||  || | ||||| |||| |  |  || |  ||  |||||||||
CTTCGTTACCATCCAACCACCACTATGACCACTCGAATAACTCACATCACAACGGCCGTCGATCGACCAGAA
480        490        500        510        520        530        540        550

        650        660        670        680        690        700        710
GTCCATTTAAACTTAGGTAACATTCGTTCTGACACATCTATTCAGTTCACGTTCTGACAACATCTATTCAAGATCGTTAACTGCAGTTACAC
| ||||| |  | |||| || ||| ||||| | | || |||  | | | || |||| || || |  || || | || ||  |  | | || |
ACCGATCCGAATCTGGGTAACATCCCACGCTTCTAATACATCCATGTTCAAACTGATTAACTGACCATGTTCAAACTGGAC
560        570        580        590        600        610        620

720        730        740        750        760        770        780
---CAGATACATTGGCATTAGATACTTCCAACATTTCGACAAGGAGTTAGACGAGACCGAGATTCAAACTTT
   | | |||  | || | ||| |  |   |||  |||  | ||   |  || || |||| ||  | ||||||
```

2. US-09-910-186A-13 (1-1400)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	= 427	Optimized Score	= 692	Significance	= 0.58
Residue Identity	= 54%	Matches	= 739	Mismatches	= 539
Gaps	=	Conservative Substitutions	= 72	Gaps	= 0

```
                    |   ||||  ||||  |  |||||||  || |  ||| | ||  |    | |||      |||  |||
          ATCAGAACATCATCTTCAACTGCTGTTATTCTGGACTTCTCGTTCTTCCGATCCGTATCCCGAATACA
                    200           210           220           230           240           250           260
380
          ACAACAAGATCGTC------AACGTTAACAGAGTAACATCCACAACTGATGAGAGCAACAACACTCCG
          | || ||||    ||       ||||    ||| |||| | |||||   |||||  ||||  || |||
          GGTTAAGATCCAAGAGTTAACAACTCTT ... AGAATAACTCTG
                    390           400           410           420           430           440
                                                                                            330
```

(DNA sequence alignment — full pairwise alignment of nucleotide sequences across numbered positions)

3. US-09-910-186A-13 (1-1400)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score   =   322   Optimized Score   =   612   Significance   = -1.15
Residue Identity   =   50%   Matches   =   682   Mismatches   =   585
Gaps   =   Conservative Substitutions =   88   0

```
100                    110  X           120  X            130           140           150           160
          CAGATGATAAATTTTAATTTCAACTACTTCAACAAGTTCTTCAAGAGAATTAAGTCTTCTTCCGTTTTAAACA
             |||||||  ||  |   |    ||  |||||||  |||  | | ||  | | ||| |   ||| |||
          ATGGCTTTCAACAAATACAACTCCTGAACAATACCTGAACACAATATCATCCTGAACC
                      X            10            20            30            40            50
```

```
1380           1390
          ACGCGTCCCGGGACTAGTGAAT
          TT
          X
```

```
CTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCA
   1050       1060       1070       1080       1090       1100       1110

   1200       1210       1220       1230       1240       1250       1260
GAACTTTAAAAATAATAATGAAAATAATATTGGGTTGTTAGGTTTCA-AGGCAGATACTGTAGTTGCTAGTA
   |-  |  |||  ||| |  ||- ||  |||| |-| | ||| ||-|-| ||   |  |  |-  |  | -|
GCTGCTGTTCAAGAAGAATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATC
   1120       1130       1140       1150       1160       1170       1180

   1270       1280       1290       1300       1310       1320       1330
CTTGGTATTATACCCACA--TGAGAGATCACCAACAGC----AATGGATGTTTTGGAACTTTATTTCTG
   |- |  |||  |    | ||| ||  ||| ||| |   |  |||| |  ||||| | |  -
TGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGTACCTGAAGGAAGTTAAACGCAA
   1190       1200       1210       1220       1230       1240       1250

        1340       1350       1360       1370       1380       1390
A---------AGAACATGGATGGCAA--GAAAAATAATAGGGATCCCGCGCCCCACCGGTCCCGGGACTAG
   |-  |||| ||| ||||| || |  ||  |  ||  ||  | ||   |||   ||  ||| |||||
ACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCCGAAAGACG-----AAGGTTGGACCGAATAG
   1260       1270       1280       1290       1300       1310       1320

       1400
TGAATTC
   |-|  |
TAACCTCTAGAGTCGAGGCCTGCAG
   1330 X    1340       1350
```

```
>O<
O||O   IntelliGenetics
>O<

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-13-inv.res made by bobryen on Thu 7 Nov 102 14:44:44-PST.

Query sequence being compared:US-09-910-186A-13' (1-1400)
Number of sequences searched:                      3
Number of scores above cutoff:                     3

Results of the initial comparison of US-09-910-186A-13' (1-1400) with:
       File : US08123975A.seq                    Complement
```

```
100-                                                           *

                                                  *
 50-
                                             *

                              *
                         *
 10-
                    *
  5-
               *

  0-  -|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
SCORE 0   5   9  14  19  23  28  33  37  42
STDEV-4  -4  -3  -3  -2  -1   0
```

```
PARAMETERS -

Similarity matrix    Unitary
Mismatch penalty     1
Gap penalty          5.00        K-tuple              4
Gap size penalty     0.33        Joining penalty      30
Cutoff score         1           Window size          500
Randomization group  0

                 SEARCH STATISTICS

Scores:    Mean    Median   Standard Deviation
           38       31          6.93

Times:    CPU                Total Elapsed
        00:00:00.00          00:00:00.00

Number of residues:         4027
Number of sequences searched:  3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                        Init. Opt.
Sequence Name   Description                 Length Score Score  Sig.  Frame
-----------------------------------------------------------------------------
1. US-08-123-975A-4  Sequence 4, Application U  1338   42    273   0.58   0
2. US-08-123-975A-1  Sequence 1, Application U  1338   42    273   0.58   0
                     **** 1 standard deviation below mean ****
3. US-08-123-975A-6  Sequence 6, Application U  1351   30    480  -1.15   0

1. US-09-910-186A-13' (1-1400)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =   42   Optimized Score         =   273   Significance =   0.58
Residue Identity  =   42%  Matches                 =   42%   Mismatches   =   384
Gaps              =   68   Conservative Substitutions =   68
```

```
                 x       10        20        30        40
              GAATTCACTAGTCCCGGACGCGTGGGCCGC---GGATCCCTATTATTTT
              ||||| |||||| | |  | |   || ||     |||||
         TTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCGGATCAAATACTTCAA
            590       600       610       620       630       640       650
 50-
              TCTTGCCATCCATGTTCTTCAGAAATAAAGTTCAAA---AACATCCATTGCTGTTGGTGATCT
              | | || |  | ||| | | || | | || ||      || ||| ||  || | |||
         TCTGTTCGACAAGACTGAACGAAAAAGAATCAGAGAAATCGTACGACCAGTCCAATTCTGGTATCCT
             660       670       680       690       700       710       720
              ----CTCATGTGGGTATAATACC--AAGTACTAGCAACTACAGTATCTGCCTTGAAACCTAACAACCCAATA
                  ||   | ||| |||    || ||||    | || ||  ||| |  |  ||||   | |  |||
         GAAAGACTTCTGGGGTGACTACCTGCAGTACGACGAAACCCTACTACATGC--TGAATCGTACGGATCCGAAC
             730       740       750       760       770       780       790
              TTATTTCCATTATTATTTTAAAGTTCAtGTGAGGTATCCGCGGTTAC--ATGTACCTGA--AAGGTCCGCGTGGT--
              |||     || ||  | |  ||||| | | |||| ||  |||| ||    |  ||      |||  |  |   ||
         AAAT---AGGTTGACGTCAACAATGTAGGTATCCGCGGTTAC--ATGTACCTGA--AAGGTCCGCGTGGT--
             800       810       820       830       840       850
250-
              AATCTGTTGCCAGAGGAGGAGATCTTGATGGTCTTCTCCTTGT-TGGTGGTAGCGGTATCAGCCATATAATGG
              |||||||     | |  |||     | || ||   ||||  |   |||| ||  |  |  |   | ||  |  -G
         --TCTGTTATGA-CTACCAACATCACCTGAACTCTTCCCTGTACCGTGGTACCGGTACCAAATTCATCATCAA---G
            860       870       880       890       900       910       920
              GAATAAGTGAGTCTTGCTAGCGACGAGGTTAATATAGACCTGATCGTTCTTTCTAACAAGGTTATCGTTAGT
              |||  || | ||  |     ||||||  || | || | | ||| | |||     ||||     | || ||
         AAATACGGTCT----------GGTAACAAGGACAATATCGTTCGCAACAATGATCGTTCGCAACAATGATCGTGTATACATC
            930            940       950       960       970       980
              AGAAGAGTTGTAACTCTTTGGATCTTAACCTTGATACCAGAGTATAATCTGTTAGCTAAAAAGAAATAGTGCT
              ||||||||       |           |   |  | |||     | ||   | |   | ||| ||| | |||||
         AATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCCAGGTGGTGTGTAGAAAAGATCTTG
            990      1000      1010      1020      1030      1040      1050
470-
              TCTGATGTTGTTAATCCTTAAAGTAGAATCCTTTCTCCCTATCAATGAAGTTGTTGGCTTTAACACGTTTAA
              |||||| |||  ||| | | ||  | || | ||| | |||||  |         |||| |  | ||||| |
         TCTGCCTCTGGAAATCCCGGACGTTGGTAATCTGCTCTC---------AGTAGTTGTAATGAAATCCAAGAA
           1060      1070      1080      1090      1100      1110
540-
              TAAGTAGTATTCCTTGTCGTAAGCAAGTAGTTACCCCAGAAGTCCTTCAAAATATTGGTGTTTAGGTTCGTT
              | |||| |    | || ||  | |  ||  |     || ||  | |    |  | | |  |||  ||  | |||
         CGACCAGGGTATCACTAACAAATCGAA--AATGAATCTGCAGGACAACAATGGTAACGATATCGCGGTTTCATC
          1120      1130      1140      1150      1160      1170      1180
610-
              GCTGTATAAAGTTGAATCCGTCTCGCTCTTAACTCCTTG-TCGAAAATGTTGAAGTATCTAATGCCAATGT
              || || | |||||| || |  || |   | |||    |    | ||| ||| | |  | |  || |
           620       630       640       650       660       670
```

2. US-09-910-186A-13' (1-1400)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

```
Initial Score      =  42    Optimized Score =  273    Significance   = 0.58
Residue Identity    = 42%    Matches         =  333    Mismatches     = 384
Gaps                =        Conservative Substitutions = 68    Gaps  = 0
```

3. US-09-910-186A-13' (1-1400)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

```
Initial Score      =  30    Optimized Score =  480    Significance   = -1.15
Residue Identity    = 41%    Matches         =  572    Mismatches     = 715
Gaps                = 101    Conservative Substitutions = 101    Gaps = 0
```

[DNA sequence alignment data — multiple aligned nucleotide sequence blocks with position numbering spanning residues 1–1400 for query and subject sequences]

```
TAACACGTTTAATAAGTAGTATTCCTTGTCGTAAAGCAAGTAGTTACCCCAGAAGTCCTTCAAAATATTGGT
| |||    || | |  | |  |  |||  |      |   ||  |||||||||||         | |||| ||
CATCACCAATAACCTGACAATCCTAAAATCTACATCAACAGGTAAACTGGAATCTRATACCGACATCAAAGA
470         480         490         500         510         520         530

600         610         620         630         640         650         660
GTTAGGTTCGTGCGTGTATAAAGTTGAATCTCCGGTCTCCGTCCTAACTCCTTGTCGAAAATGTTGAAGTATCT
| ||| | || ||  || | |  ||| |||  | || ||  |   || |  ||| | |||| || | |||| ||
CATCCGTGAAGTTATCGCTAACGGTGAAATC-----ATCTTCAAATGGACGGTGAACATCGAT--CGTACC-
540         550         560         570         580         590         600

670         680         690         700         710         720         730         740
AATGCCAATGTATCGTAACGCAGTTAACGACATCTTGAATAAGATGTGTCAGAAACGTGAAATGTTACC
  ||| |||  ||  | ||||  ||| ||  ||  |||| |||| |  |||  |  ||| | || |||
----CAGTCATCTGGATGAAAT--ACTTCTCCATCTTCAACACCACGAACTGTCTCAGTCCAATATCGAAGA
610         620         630         640         650         660

750         760         770         780         790
TAAGTTTAAAATGGACTTTTGGT-CGATTAAGTTA------------CCGTTAATGTAAAGCTTAGA
||  ||| || | ||  | |||| | ||| ||||         | ||| || || ||||| |||||| ||
ACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGTGAIGTACAACAAAGA
670         680         690         700         710         720         730         740

800         810         820         830         840         850         860
GTCACCTAATCTGTCGTTAGTGATGAGTGACGAAAATCC--ACTTGTTGATGTAGTCAGAAATACCGTTTGCG
| | || |||  |||  |   | | |  |  |||| |||| ||||| |||| |||  || | | ||||| || |
----ATACTATATGTTCAATGCTGGTAACAAGAACTCTTACAAGAACTGAAGAAGACTCTCCGGTTG--
750         760         770         780         790         800

870         880         890         900         910         920         930
TTACCCGTAGTTGAATGCTAACTTTGGTTAAATACCTGC-GTTGCTTCTTGCAAGGTCCAAATGATCTCGTTGTG
 |||||| || |||  | |  || ||||| || ||  || |||| || | || || | ||| |    || |||
------GTGAAATCCTGACTCGTTCGTTCCAAATACAACCAGAACTCTAAATACAACTACCGCGGACCTGTA
810         820         830         840         850         860

940         950         960         970         980         990         1000
GTTAAGAGAGACCTTC--CAACCGGAGTTGTTGT--CTCTCATACAGTTGATGATAGTGTACTCGTTGTTAA
|||  | | | |  ||      ||| ||| ||  |  || | |  | || |||  ||    || | |||||
CATCGGTGAAAGTTCATCATCCGTCGCAAATCTAACTCAATCTAACTTCAGTCCATCAATGA---TGACATCGTACGTAA
870         880         890         900         910         920         930

1010        1020        1030        1040        1050        1060        1070
CGTTGACGATCTTGTTGTCGTAGTTAGGAATCCTGACCCCAGAAGAATATAGAGAAGTTCTTGTACTTGTTGT
|| |  || ||| |   || || ||| | |||| || |  ||| ||||  || |||||| | |||| ||| | |
AGAAGACTA-CATCAACTACCTGGACTTCTTCAACCTGGATCAGGAATGGCGTGTATACACCTACAAGTACTTCA
940         950         960         970         980         990         1000

1080        1090        1100        1110        1120        1130        1140
CGTAGATAAGTAGTCGTTTGAGAGATGTTGACCTCGGAAAGCTTGTCGTTGTAGATACCGAATTGGTTTT
|| |  | | |  | |  |   |||  ||||  || || |||  |||||  ||| ||||||| ||  | |
AGAAAGAAGAAGAAAGCTTTCCGGCTCCGATCTCTGATTCCGACGAACTCTACACACCAGAATCCAGATCA
1010        1020        1030        1040        1050        1060        1070        1080

1150        1160        1170        1180        1190        1200        1210
TGTTAGTTGGGTACTTGTACACGTACATCTGTAGTAGAAG-AAAGCTTAAAAGGAATACTTATTATTTAGGGTATCAGTTACCAT
|| | ||| |  |||| | ||  |  | |  ||| |  ||| |||| |||  || ||  |  |  ||  ||| | || |||| |
AAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGACGTCGTAACCGGAA-GTGTCGACGTAT
1090        1100        1110        1120        1130        1140        1150

1220        1230        1240        1250        1260        1270        1280        1290
TTATCATTCTTGTATCTGTATCCATGTTTTAAAACGGAAGAAGAGACTTAATTCTTCTTGAAGAACTTGTTGAAGTAGGAA
| || |  |  || ||  |||| | ||  |   || || ||  |   ||  |  || | ||  |||| |  || |   |  |
TCGGTTCGATCGGTATCCACCGTTTCTACGAGTCGTATCCGGAATCTACGACGAAAGATGAAGAACTACTGACGAAA
1160        1170        1180        1190        1200        1210        1220

1300        1310        1320        1330        1340        1350        1360
ATTAAAATTTTATCATCTGTATAGGAAG-AAAGCTTAAAAGGAATACTTATTATTTAGGGTATCAGTTACCAT
| | ||  | |  | ||| ||| ||  || |||| |||  || ||  |  |  ||  ||| | |||| |||||
TCTCCAA----ATGGTACCTGAAGGAAGTTAAACGCAAACCGTACAACCGTACAACTGGGTTGCAATTGGCAG
1230        1240        1250        1260        1270        1280        1290

1370        1380        1390        1400
AGAATTTAG-TTCTTGCTGACTCCTCTCCCCATGGTGAATTC
```

```
||  | ||||||||||||||   |||    | |||  |||||  |||  | ||||||| ||
TTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAGTAACCTCTAGAGTCGAGGGCTGCAG
1300        1310        1320        1330 X      1340        1350
```

```
> O <
OI |O   Intelligenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-14.res made by bobryen on Thu 7 Nov 102 14:34:07-PST.

Query sequence being compared:US-09-910-186A-14 (1-449)
Number of sequences searched:          3
Number of scores above cutoff:         3

Results of the initial comparison of US-09-910-186A-14 (1-449) with:
File :US0812397SA.pep
```

Histogram (Number of Sequences vs SCORE / STDEV):

```
100-
   -
   -
 50-
   -
   -
   -
   -
 10-
   -
   -
  5-
   -
   -
   -
   -
   -                                              *
   -                                              *
  0 ----------------------------------------------------
      |    |    |    |    |    |    |    |    |    |
SCORE 0   18   35   53   70   88  105  123  140  158
STDEV               -9   -8   -7   -6   -5   -4   -3  -2  -1  0
```

```
               PARAMETERS

Similarity matrix    PAM-150    K-tuple              1
Threshold level of sim.  16%
Mismatch penalty     1          Joining penalty     20
Gap penalty          5.00       Window size        449
Gap size penalty     0.05
Cutoff score         0
Randomization group  0

               SEARCH STATISTICS

Scores:      Mean     Median     Standard Deviation
             153      144        8.66

Times:       CPU                 Total Elapsed
             00:00:00.00         00:00:00.00

Number of residues:              1704
Number of sequences searched:       3
Number of scores above cutoff:      3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-5	Sequence 5, Application U	439	158	247	0.58	0
2. US-08-123-975A-2	Sequence 2, Application U	850	158	271	0.58	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-3	Sequence 3, Application U	415	143	276	-1.15	0

```
1. US-09-910-186A-14 (1-449)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    = 158   Optimized Score           = 247   Significance = 0.58
Residue Identity = 31%   Matches                   = 141   Mismatches   = 233
Gaps             =       Conservative Substitutions = 35                = 34

         20        30      X 40        50        60        70        80
NNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGDVYKYPTNKNQFGIY
                  |||       ::|||:|||              |||              ||||
              FNKTYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGV--ELNDKNQFKLT
             X        10        20        30          40        50

  90       100       110       120       130       140       150
NDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN--VNNEYTIINCMRDNNSGWKVSLNHNEIIW
  :|:||                |||:||:||| |:|:|:||    ||||||||||| |:|||:|||||||||
SSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMK-NNSGWKISIRGNRIIW
     60        70        80        90       100       110       120

 160       170       180       190       200       210       220       230
TLQDNAGINQKLAFNYGNANGISDYINKWIFVTTNDRLGDSKLYINGNLIDQKSILNLGNIHVSDNILFKI
||:|                 :|:|||:|||| ||||   :|||||||| |||||  |:||||:|:|:||
TLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKL
   130       140       150       160       170       180       190

   240       250       260       270       280       290       300
-VNCSYTRYIGIRYFNIFDKELDETEIQTLYSNEPNTNLKDFWGNYLLYDKEYYLLNVLKPNFIDRRKDS
  :|:||||  |  ||   | |  |:  :|   ||||::|:|||||:|  :||||:|||||:||||:|||:
DGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKPYYMPNAGNKNSYIKLKKDS
  200       210       220       230       240       250       260

  310       320       330       340       350       360
TLSINNIRSTILLANRLYSGIKVKI------QRVNNSSTNDNLVRKNDQVYINFVASKTHLFPLYADTATT
  ||          ||        |         :|    || |    |||:||  ::||| |||
PVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYVYKYFKK
   270       280       290       300       310       320       330

   370       380       390       400       410       420
NKEKTIKISSSG----NRFNQVVVMNSVGNNCTMNFKNNNGNNIGLLGFKADTVVASTWYYTHMRD----
 :||          |:          :|:  :|         | ||:    ::|:|||:|||:
EEEKLFLAPISDSDFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEICLGIHRFYESGIVPEEYKDYFCIS
  340       350       360       370       380       390       400

                                    X
      430        440
------HTNSNGCFWNFISEEHGWQEK
               X
KWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
 410       420       430        X
```

```
2. US-09-910-186A-14 (1-449)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    = 158   Optimized Score           = 271   Significance = 0.58
Residue Identity = 32%   Matches                   = 155   Mismatches   = 254
Gaps             =       Conservative Substitutions = 35                = 35

             X        10        20        30        40        50
             MGESQQELNSMVTDLNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNM
                                   :||  |||||||:|||  |||:||| |||::|
DFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTTLIIEMPNKYNSEILNNIILNL
   360       370     X 380       390       400       410       420
```

```
                         390        400        410        420        430        440
VVVMNS-----VGNNCTMNFKNNNGNNIGLLGF---KADTVVASTWYYTHMRDHTNSNGCFWNFISEEHGW
|||||     ||||| :| |||| |||| ||        ||| |||:|| ||||||||||| :| ||
VVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRPTLGCSWEFIPVDDGW
340        350        360        370        380        390        400        410

     X
QEK
|-|:
GERPL
    X
```

```
        60         70         80         90        100        110        120
RYKNDKYVDTSGYDSNININGDVYKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYD
|||  ||| ||  ::  : |||::||||||||||   |::   ||:::  ||  :: ||  |||||:||| |
RYKDNNLIDLSGYGAKVEYDGV--ELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYK
430        440        450        460        470        480        490

        130        140        150        160        170        180        190
NKIVN--VNNEYTIINCMRDNNSGWKVSLNHNEIIWTLQDNAGINQKLAFNYGNANGISDYINKWIFVTITN
|  :    ||||||||||: ||||||: ||  ||||| | ||| |   |  :| | |   |:||: |||||||
NDGIQNYIHNEYTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITN
500        510        520        530        540        550        560

        200        210        220        230        240        250        260
DRLGDSKLYINGNLIDQKSILNLGNIHVSDNLLFKI-VNCSYTRYIGIRYFNIFDKELDETEIQTLYSNEPN
  ||:||||||| | :| | | ||||| | ::|||   :| | |  |||:|: |||:||| :|| ||: | |
N-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEBRYKIQSY
570        580        590        600        610        620        630

        270        280        290        300        310        320        330
TNILKDFWGNYLLYDKEYLLNVLKPNNFIDRRKDSTLSINNIRSTILLANRLYSGIKVKI------QRVN
   |||||||  : :|||   :  :| ||       |:   :: |  | |||| | |  |        |||
SEYLKDFWGNPLMYINKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSN
640        650        660        670        680        690        700        710

        340        350        360        370        380        390
NSSTNDNLVRKNDQVYINFVASKTHLFPLYADTATTNKEKTIKISSSG-----NRFNQVVVMNSVGNNCTMN
 |: || :|||:|  |   |::   :  |   |:  ::|:|  :| |           | ||| : ||| :
SQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEVDEQPTYSCQIL
720        730        740        750        760        770        780

        400        410        420        430        440
FKNNNGNNIGLLGFKADTVVASTWYYTHMRD------------HTNSNGCFWNFISEEHGWQEK
|| :  | ||:||     | | : |  : |              | |:|| |||||  || :|
FKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
790        800        810        820        830        840        850
```

3. US-09-910-186A-14 (1-449)
    US-08-123-975A-3 Sequence 3, Application US/08123975A

```
Initial Score    =   143   Optimized Score  =   276   Significance  =  -1.15
Residue Identity  =   44%   Matches          =   185   Mismatches    =   192
Gaps              =   20    Conservative Substitutions  =   18
```

```
              40         50    X    60         70         80         90        100
LISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGDVYKYPTNKNQFGIYNDKLSEVNISQNDYII
                  ||  :|  |||||||||||| |:|||:| ||||||||||||||:|
              RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
X          10         20         30         40         50

        110        120        130        140        150        160        170
YDNKYKNFSISFWVRIPNYDNKIVNVNNEYTIINCMRDNNSGWKVSLNHNEIIWTLQDNAGINQKLAFNYGN
|:  | ||| ||||:|||:| |:| |||||||||||  ||||||||||: ||||||||:    |||: |:|
YNSMYENFSTSFWIRIPKYFNSI-SLNNEYTIINCM-ENNSGWKVSLNYGEIIWTLQDTQEIKQRVFKYSQ
60        70        80        90        100        110        120

        180        190        200        210        220        230        240
ANGISDYINKWIFVTITNDRLGDSKLYINGNLIDQKSILNLGNIHVSDNILFKIVNCSYT-RYIGIRYFNIF
   |||||||:||||||||:||  ||:||||:||||| | |||||| |:|  :  | |   ||| |:|||:|
MINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNIMEFKLDGCRDTHRYIWIKYFNLF
130        140        150        160        170        180        190

        250        260        270        280        290        300        310
DKELDETEIQTLYSNEPNTNILKDFWGNYLLYDKEYLLNVLKPNNFIDRRKDSTLS------INNIRST
||||:|:||: || :|   ||LKDFWG:|  |||  :|:|  || :           |   :  :::
DKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTN
200        210        220        230        240        250        260

        320        330        340        350        360        370        380
ILLANRLYSGIKVKIQRVNNSSTNDNLVRKNDQVYINFVASKTHLFPLYADTATTNKEKTIKISSSGNRFNQ
| |::|| | |:| |: :      || :|::|| ||| | :| : | |  :     : :: |:     |
IYLNSSLIYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ
270        280        290        300        310        320        330
```

```
> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-15.res made by bobryen on Thu 7 Nov 102 14:45:08-PST.


Query sequence being compared:US-09-910-186A-15 (1-1317)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

Results of the initial comparison of US-09-910-186A-15 (1-1317) with:
     File : US08123975A.seq
```

```
100-
      -
N  50-
U     -
M     -
B     -
E     -
R     -
      -
O     -
F  10-
      -
S     -
E   5-
Q     -
U     -
E     -
N     -                                               *
C     -
E     -                                          *
S   0-------------------------------------------------|--|--|--|--|
SCORE 0     63    126   189   252   315   378    441   504   567
STDEV                                             -9  -7  -5  -3  -1
```

```
              PARAMETERS

Similarity matrix      Unitary
Mismatch penalty       1           K-tuple              4
Gap penalty            5.00        Joining penalty      30
Gap size penalty       0.33        Window size          500
Cutoff score           1
Randomization group    0

              SEARCH STATISTICS

Scores:      Mean      Median      Standard Deviation
             558       542         15.01

            CPU                    Total Elapsed
Times:      00:00:00.00            00:00:00.00

Number of residues:              4027
Number of sequences searched:       3
Number of scores above cutoff:      3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
Sequence Name       Description                                              Length  Init.  Opt.    Sig.  Frame
                                                                                     Score  Score
------------------  -------------------------------------------------------  ------  -----  -----  -----  -----
1. US-08-123-975A-4  Sequence 4, Application U                                1338    567    777    0.60   0
2. US-08-123-975A-1  Sequence 1, Application U                                1338    567    777    0.60   0
                     **** 1 standard deviation below mean ****
3. US-08-123-975A-6  Sequence 6, Application U                                1351    541    675   -1.13   0
```

```
1. US-09-910-186A-15 (1-1317)
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score   =   567    Optimized Score   =   777    Significance  =   0.60
Residue Identity =  60%    Matches           =   813    Mismatches    =   473
Gaps            =    0     Conservative Substitutions =    59
```

```
                10        X  20        30        40        50        60        70
     GAATTCACGATGTCCTACCACCAGACAAGAGATCCTGATCTTGTACTTCAACAAGCTGTACAAGAAGATCAAG
                          ||   ||||  || |   |||||||| ||||||||| |||||     ||
              CTCGAGCCATGGCTCG--TCTGCTGTGTTACCTTCACTGAATACATCAAGAACATCATC
                          X        10        20        30        40        50

      80        90       100       110       120       130       140
     GACAACTCCATCTTGGACATGAGATACGAAAACAATAAGTTCATGCGACATCTCCGGTTACGGTTCCAACATC
     | |||||||  ||  | ||||  |  |  ||||| |||||   ||  |||| ||||| |||||| ||||||||
     AATACCTTCCATCCTGAACCTGCGCTACGAATCACCTGATGCGACCTGTCTCGCTACGCTTCCAAAATC
      60        70        80        90       100       110       120

     150       160       170       180       190       200       210
     TCCATCAACGGTGCACGTCTACATCTCCACCAATGAAAACCAGTTCGGAATCTACTCCTCCAAGCCTTCC
     ||||   ||    |||| | ||||| |||| |||  || |||  ||| ||||| ||||||||||||||||
     AACATCCGGTTCTAAAGTTAAC TTCGATCCGATCGCAACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCC
     130       140       150       160       170       180       190       200

     220       230       240       250       260       270       280
     GAGGTCAACATCGCTCAGAACAAGACATCATCTACACGGAAGATACCAGAACTTCTCCATCTCCTTCTGG
     |||| || ||| || |||| || |||| | ||| |  || |||  ||||  |||||||||||||||||||
     AAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTGACGAAAAACTTCTCCACCTCCTTCTGG
     210       220       230       240       250       260       270

     290       300       310       320       330       340       350       360
     GTCCGTATCCCAAAGTACTTCAACAAGGTCAACCTGAATAACGAGTACACCATCGACTGACATCCGTAAC
                || ||| |||||  |||||  |||| | |||  |||  ||||  ||||||  ||||||||| ||
     ATCCGTATCCCGGAAATACTTCAACTCTCGTGAACAACAATGCACATACACAACTCAACTGCATGGAAAAC
     280       290       300       310       320       330       340

     370       380       390       400       410       420       430
     AATAACTCCGATGGAGAGATCTCCCTGAACTACAACAAGATCATCTGGACCCTGCAGGACACCGGCGGGTAAC
     |  ||| || | ||||  |||||| |  |||| |||| ||||  | |||| |||| |||||||||  ||||||
     ACCATCACCAACAATCGTCTGAACTAACTCACATAAAATCTACACTCAACGGCGTCTGGACTCATGGGACACTCAGGAAATC
     490       500       510       520       530       540       550
```

```
     440       450       460       470       480       490       500
     AATCAGAAGTTGGTCTTCAACTACACCAGATGATCTCCATCTCCGACTACATCAACAAGTGGATCTTCGTC
     || |||  |  || ||| |||| | | |||| | || ||| |  ||| |  || || ||| |   ||||||
     AAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTGAGATCGCTGGATCTTCGTT
     420       430       440       450       460       470       480
```

```
     510       520       530       540       550       560       570
     ACCATCACCAATAACCGTTTGGGAAACTCCAGAATCTACATCACGGTAACTGATCGACGAGAAGTCCATC
     |||||  | | ||   |  || ||| || ||| ||||  || |  |||  ||||| | ||||| |  ||||
     ACCATCACCAACAATCGTCAGAATAACTACAAAATCTCCAAAATCTACACTAACGGCGTCTGGACTCACCGC
     490       500       510       520       530       540       550
```

```
     580       590       600       610       620       630       640
     TCCAACTTGGGTGACATCCACGTCTCCGACAACACATTTGTTCAAGATCGTCGGTTGTAACGACAC---CCGT
     ||||| || || || | || |  | | || ||||   |||  |||  || |  || | |||  ||||  ||||
     TCCAATCTGGGTAACATCCACGTTCTCTAATAACATCATGTTCAAACATCATCAAACTGGACAGTGTCGTCAATAACTCACCGC
     560       570       580       590       600       610       620
```

```
     650       660       670       680       690       700       710
     TACGTCGGGAACTTGACTTGACTTCAAAGTCTTCGACACTGAGTGGTAAGACCGAGATGGATCGGAGATCGAGACTTGTACTCC
     ||| ||||   |  |||||   || ||  |  | |||||  |||  | | |||| |  ||||||||| ||| |  |
```

2. US-09-910-186A-15 (1-1317)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score = 567   Optimized Score = 777   Significance = 0.60
Residue Identity = 60%   Matches = 813   Mismatches = 473
Gaps = 59   Conservative Substitutions = 0

```
3. US-09-910-186A-15 (1-1317)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =  541   Optimized Score        = 675   Significance = -1.13
Residue Identity =  548   Matches                = 734   Mismatches   =  529
Gaps             =   90   Conservative Substitutions =  90               0
```

Sequence alignment printout — the remainder of the page consists of dense paired nucleotide sequence alignment blocks with position numbering (e.g. 270, 280, 290 ... 1200) and match bars (|) between the two aligned strands.

```
TGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTCGATCGGTATCCACCGTTCTACGAATCTG
1120     1130      1140      1150      1160      1170      1180

1210      1220      1230                                        1240
GTCGCTTCCTCCTGG--TACTACAACACATCCG----------------------------TAAGAACACCT
||--|-|||---|||--||||-||||-||||||                            ||| ||
GTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAAAC
1190      1200      1210      1220      1230      1240      1250      1260

1250                                                             1310
CCTCCAAC--------GGTTGCTTCTGGTCCTTCATCTTCCAAGGAGCACGGTTGGCAGGAGAACTAATAGG
|-|-||||        |||||||||-|||--||||||-|-||||||||-||||-||-|-||||
CGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTC
1270      1280      1290      1300      1310      1320      1330

       x
AATTC
       |
TAGAGTCGAGGCCTGCAG
  1340      1350
```

```
> O <   IntelliGenetics
O| |O
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-15-inv.res made by bobryen on Thu 7 Nov 102 14:45:24-PST.

Query sequence being compared:US-09-910-186A-15' (1-1317)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-15' (1-1317) with
    File : US08123975A.seq

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	40	336	0.58	0
2. US-08-123-975A-4	Sequence 1, Application U	1338	40	336	0.58	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	28	200	-1.15	0

1. US-09-910-186A-15' (1-1317)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score = 40	Optimized Score = 336	Significance = 0.58	
Residue Identity = 40%	Matches = 409	Mismatches = 518	
Gaps =	Conservative Substitutions = 74	Gaps = 0	

```
                    X         10        20        30        40        50
              GAATTCCTATTAGTTCTCCTGCCAACCGTGTCCTTGGAGATGAAGGACCAG
              |||||||  ||||||||||||||||||||||||||||  |||||
TCTGGTTGGAAAGTATCTGAACTACGGTGAAATCATCTGGACTCTG-----CAGGACACTCAGGAAATC
350       360       370       380       390       400       410

        60        70        80        90        100       110       120
AAGCAACCGTTGGAGAGGAGGTGTCTTACGGATGTTGTGTAGTAGTACCAGGAGGAAGCGACCAAGTTGTTGGAG
             |||||    |||||
AAACAGGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACAATCGCTGGATCTCGTT
420       430       440       450       460       470       480

       130       140       150       160       170       180
TGGAAACCCAACAAACCGATGTTCCACCGTTGTTGTCTGGAA------GTTCATGGTACAG---TTATT
                       |||             ||||               |||
ACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAAGCGCCGTCTGACCAGAAACCGATC
490       500       510       520       530       540       550

       190       200       210       220       230       240       250
ACCGATGGAGTCCATGACGATGATTGTCCCAGAGAGTGTTGAGATTAGAGGTACGGATCAGCTTGATGAT
          |||||      |||               |||
TCCAATCTGGGTAACATCCAGCTTCTAATAACATCATGTCAAACTGGATCGTGTGTGGACACTCACCGC
560       570       580       590       600       610       620

260       270       280       290       300       310       320       330
CTTTTCAGGTTTGGCATAGAGAATATCGGCGTACAGACGGTATTCGACATTCTCTGCGACAACGTTGATGTA
        |||||          |||              |||              |||
TACATCTGGATCAAATACTTCAATCTGTTCGACAGAGAACTGAACGAAAGAATACAAAGAACCTGTACGAC
630       640       650       660       670       680       690       700

340       350       360       370       380       390
AGCCAGATCGTTCTTTCTGAC---GAAGTTATCGGTGTTGGAAATAT-CAGTA---GATCCGTTCTTTCTG
             |||              |||              ||||
AACCAGTCAATTCTGTATCCTGAAAGACTTCTGGGGTACTACCTGCACTACGACACAAACCGTACTACATG
710       720       730       740       750       760       770

400       410       420       430       440       450       460
ATAATGACCTCGACTCCGGTGTACAATCTGGTGTTGGAGAGAGGTTTGGCTTCTGGTAGA--CACCTCTCT
             |||              |||              |||
CTGAATCTGTACGATCCGAACAGACATAGTTGAGCGTCAACATGTAGGTATCCGCGGTTACATGTACCTGAAA
780       790       800       810       820       830       840

470       480       490       500       510       520
GCTGGTTGATGTTC----AAGAAGTTGGAGTTCTGGGTGATGGACTTGTCGGTAC----GCAACAAGTTCAG
             |||              |||              |||
GGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGA-ACTCTTCCCGTACCGTGTACCGTGTACCAAATTCAT
850       860       870       880       890       900       910

530       540       550       560       570       580       590
CAAGTAGTAACGTTTGT-TGTACAGCAGGTAGTTACCCCAGAGAGTCCTTCAGGATGGATGGGTCAGGCTCGT
             |||              |||              |||
CATCAAGAAAATACGGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGT
920       930       940       950       960       970       980

600       610       620       630       640       650       660
CGGAGTACAAGGTCTCGATCTCGGTCGTTACCCAACTCAGTGTCGGAAGACTTTGAAGTAAGTAACGGA
             |||              |||              |||
------CGGAGTACAAGGTCTCGATCTCGGTCGTTACCCAACTCAGTGTCGGAAGACTTTGAAGTAAGTAACGGA
```


(handwritten annotation: "complement")

```
100-
   -
   -
   -
 N -
 U 50-
 M -
 B -
 E -
 R -
   -
 O -
 F 10-
   -                                           *
   -
 S -
 E 5-                            *
 Q -
 U -
 E -
 N -                  *
 C -
 E -
 S 0---|---|---|---|---|---|---|---|---|---|
SCORE 0   -4   9   13   18   22   27   31   36   40
STDEV     -4   -3   -2   -1   0
```

PARAMETERS

Similarity matrix	Unitary
Mismatch penalty	1
Gap penalty	5.00
Gap size penalty	0.33
Cutoff score	0
Randomization group	0

K-tuple	1
Joining penalty	4
Window size	30
	500

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	36	29	6.93

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
AGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAGAT---CTTGTCTGC
990        1000       1010       1020       1030       1040       1050
     ||||      ||| |   |||||||   |||||||| ||||  ||||||||||||   |||||||||
AACCAGTTCCAATTCTGGTATCCTGAAAGACTTCGAAAGATTACCTGCAGTACGACAAACCGTACTACATG
          710        720        730        740        750        760       770

TCCCGACGTAACGGGTGTCGTTA---CAACCGACGATCTTGAACAAAATGTGTCGGAGACGTGGATGTCAC
   670        680        690        700        710        720        730
|||||||||||   ||||| ||     |||||||||||||||||  |||||||||||  |||||||||||||
ATAATGACCTCGACTCCGGTGTACAATCTGTGTTGGAGAAGATGTTGGCTTCGTTCTTGGTAGA--CACCTTCT
      400        410        420        430        440        450       460

TCTGGAAATCCCGACGTTGGTAATCTGTCCAGTGAGTAGTCGGAGATGGGATCATCTCGGGTTCAGAGTT
1060       1070       1080       1090       1100       1110       1120
||||||||||||       ||||||||||     |||    |||||||||||||||   ||||||||||||
CTGAATCGTGACGATCGGACAAAATACGTTGACGTGTCAACAAATGGAGGTATCCGCGGGTTACATGTACCTGAAA
       780        790        800        810        820        830       840

--CCAAGTTGGAGATGGA-CTTCTCCTCGATCAAGTTACCGGTTGCGGTTGTGTGTAGAAAGAT---1050
   740        750        760        770        780        790        800
   |||||||||||||    ||    |||||||||| |||   |||||| |||||||||  |||||
GCTGGTTGATGTC----AAGAAGTTGGAGTTCTCGGGTGATGGGACTTGTCGGTAC----GCAACAAGTTCAG
       470        480        490        500        510        520       910

TAACAATGCAAAAGAATTGCAGGACAACAAATGGTAAC---GATATCGGTTTCATCGGGTTCCACCAGTT
1130       1140       1150       1160       1170       1180       1190
|||| |||||||||||||||||||||  ||||||        ||||||||||||||||||  ||||||||
GGTCCGCGTGGTTCTGTTCTTGATGGTTCTCGGTGATGAGGACTTGTCGGTAC-ACTCTTCCCTGTACCGGTTGGTACCCAAAATTCAT
      850        860        870        880        890       900        910

TATTGGTGTGACGAAGATCCACTGTGTGATGTCGGAGATGGGATCATCTCGGGTGTAGTTGAAGA
810        820        830        840        850        860       870
|||||||| |||||||  ||||||| ||||||||||||||||||||  ||||||||||||||||
CAAGTAGTAACGTTGT-TGTACAGCAGGTAGTTACCCCAGAAGTCCTTCAGGATGGAGGTTCAGGCTCGT
  530        540        550        560        570        580       590

CAACAATATCCCTAA-------ACTGGTTGCTTCCAACTGGTACATCGTCAGATCG--AACGTTCCTCT
1200       1210       1220       1230       1240       1250
||||||||| ||          |||||||   |||||||||||   |||||||     ||||||||
CATCAAGAAATACGCCGTCTGCTGCTACCAATCTCGCTACCAATGTCTGCCAATCTCGTGTTATCAATGTTGT
 920        930        940        950        960        970       980

CCAACTTCTGATTGTTACGGCGGTGTTCCTGCAGGTCCAGATGATCTCTGTTGTACGGAGGAGATCTTCC
880        890        900        910        920        930       940
    ||||||| |||||||| |||||||||||||   ||||||||||||||    |||||||||||
CGGAGTACCAAGGTCTGTCGTTA---CAACCGACGATCTTCGTTGTGTCGGAGAAAAAATGTTGTCGGAGACGTGGATGTCAC
    600        610        620        630        640        650       660

CGCCACTCGGGTTGCTCTTCGGGAGT-TCATCCCGGTTGATGACCGGTTAAC---AACGTTCCGCGTAAC----
1260       1270       1280       1290       1300       1310       1320
|||||||||| |||||||||||||| |||||  |||||| |||||| |||||
AGTTAAGAACAAAGAATACCGTCTGGCTGTTGGTAATCTGTATGAATGAAACGACGAGGGTATCAC
 990       1000       1010       1020       1030       1040       1050

ATCCGGAGTTATTGTTACGGATGCGAGTCGATGA
950        960        970
  |||||||| |||||||||||
-CCGGGAAAGCTT
1330
X

2. US-09-910-186A-15' (1-1317),
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    = 40    Optimized Score        = 336    Significance = 0.58
Residue Identity = 40%   Matches                = 409    Mismatches   = 518
Gaps             = 74    Conservative Substitutions = 0

                  X       10        20        30        40        50
                  GAATTCCTATTAGTTCTCGTCGCCAACGTGTCCTTGGAGATGAAGGACCAG
                        ||||||||  |||      |||||||  |||||||||||||
TCTGGTTGGGAAGTATCTCTGAACTACGGTGAAATCATCATCGAGAAATC------CAGGACACTCAGGAAATC
350        360        370        380        390        400       410

AAGCAACCGTTGGAGGAGGTGTTCTTACGGATGTGTTGTAGTACCAGGAGAAGCGACCAAGTTGTTGGAG
60         70         80         90        100        110       120
 |||||||||||||||  ||||||||||| ||||||||| ||||||||||||||   ||||||||||
TGGAAACCCAACAACAACGATCTGCGAGAATAACTTCAAATGTGTTGCACAATCGCTGACTGACCTTCGTT
420        430        440        450        460        470       480

ACCATCACCAACAATCGTCTGCGAATAACTCCAAAATCTCACATCGTCAGGCGCCGTCGACGAAACCGATC
130        140        150        160        170        180
 ||||||||||||||  ||||     |||||||  |||||  |||||||||||||  |||||
TGGAAACCCAACAACAACGATGTTCCACCGGTTTCCACCGTGTTGTTCTGGAA-----GTTCATGGTACAG----TTATT
490        500        510        520        530        540       550

ACCGTGGAGCCATGGCAGGATGATGGCGTTGTGCCCAGAGAGTTGTTAGAGGTACGGATCCAGCTTGATGAT
190        200        210        220        230        240       250
|||||||||  |||||||||||||||  |||||||  |||||||||||||||  ||||||
TCCAAGTCCTGGTAACGTCCATCCACCACGCTTCTAATAACATCATGTTCTAAACTGGACCTGTCCTGACACTCACCGC
560        570        580        590        600        610       620

CTTTTCAGGTTGGCGATAGAGATACGGCGTACAGACGGTACAGACATCTTCGTCGCAACGTTGATGTA
260        270        280        290        300        310       320
|| |||||| ||||  || |||||||   ||||||  ||||||||||| |  |  ||||||||||||
TACATCTGGAATCAAAATACTTCAAATCTGTTCGACAAAGAACTGAACAGAAGAAAAGAACCTGACGTTACGAC
630        640        650        660        670        680       690

CTTTTCAGTTGGCGATAGAGATATCGGCGTACAGACGGTACAGACATCTTCGTCGCAACGTTGATGTA
330
  ||||||||||     |||||  |||||||| ||||    ||||||||
AGCCAGATCGTTCTTTCTGAC---GAAGTTATCCGGTGTTGGAAATAT-CAGTA---GATCCGTTCTTTCTG
340        350        360        370        380        390
```

```
TGATGTAGTCCGAGATGGAGATCATC--TGGGTGTAGTGAAGACCAACTTCTGATTGTTAC--CGGCGGTG
||·||··||·||·||·||·||·||  ·||·||·|·| ·||·||||·||·|||  · ||·||| |||·|||·||
TGCGTTACAAAGACAAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
        60        70        80        90       100       110       120

900      910       920       930       940       950       960
TCCTG-----CAGGGTCCAGATGATCTTGTTGTTGTAGTTCAGGGGAGATCTTCCATCCGGAGTTATTGTTACGGA
|||·     |||||·|||| ||··| ·|| ·|||·|·|   ·|||·|·||·||||| ||||·||·|· ||·||
AACTGAATGACAAGAACCAGTTCAAACTGACCT-CTTCCGCTAACCTGACCTCTGTTACT-----CAGA
        130       140       150       160       170       180       190

970       980       990      1000      1010      1020      1030
TGCAGTCGATGATGGTGTACTCGTTATTCAGGTTGACCTTGGTGAAGTACTTTGGGATACCGGACCCAGAAGG
|||·|· ·||·||·|· ·||||·|||·|| ||·||   ·||·|·|||·|| ·|||· ·||·||·|||·|||  ·
ATCAGAACATCATCTTCAACTCCGTATTC---CTGGACTTCTCTGTTTCCTTCTGAATCCGTATCCCGAAAT
260       200       210       220       230       240       250

1040      1050      1060      1070      1080      1090      1100
AGATGGA-GAAGTTCTCGTATCTTCCGTTGTAGATGATGTCGTTGTTCTGAGCCGATGTTGA-CCTCGGAAGG
|·|·| ·||·|· ·||| ·|·||·|| ||·||·||||||·||·|·|| ·|| || ·|| |·| || ·|||·|
ACAAGAACGACGGGTATCCAGAATTACACCACACATGAATACACCATCATGCATGAAGAATAACTCTG
260       270       280       290       300       310       320       330

1110      1120      1130      1140      1150      1160      1170
CTTGGAGGAGATCTCCATCCGCGGTAACCTGGTTTCTATTGGTGGAGTAGACGTCACCGTTGATGGAGATGTT
|||||·|| |||·  ·||||· ·|||·||·||·|| ·|| ·|| ||·||·|| ·||·|· || ·||·|| ·|
GTTGGAAGATCTCCATCCGCGGGTAACGGGTATCCAGGACT-CTGATCGAATATCAACGGTAAGACCAAATCT
340       350       360       370       380       390       400

1180      1190      1200      1210      1220      1230      1240      1250
GGAACCGTAACCGGAGAGATGTCGATGAACTTATTGTTTCGTATCTCATGTCCAAGATGGAGTGTGTCCTTGAT
|·| · ·||·|||||·||·||·|||·|  |·|| ·||| ·|· ||· |·|· ||·|| ·|||·|·|| ·||
GTATTCTTCGAATACAAACATCCGTGAAGACA-TCTCTGAATACATCAATCGGCTGGTTCTTCGTTCCATCAC
410       420       430       440       450       460       470

1260      1270      1280      1290      1300      1310      X
C---TTCTTGTTACAGCTTGTTGAAGTACAAGATCAGAGATCTTGTCGTTGGTGTAGGACATCGTGAATTC
    ·|·|| ·|||·|| ·||| ·|·|| ·|||· ||· ||  ||||||· ·
CAATAACCTGAACAATGCTAAAATCTACACACGGTAAACTGGAATCTAATACCGACCATCAAAGACATCCG
480       490       500       510       520       530       540 X

TGAAGTTATCGCTAACG
550       560
```

```
> o <
o| |o   IntelliGenetics
> o <
        FastDB - Fast Pairwise Comparison of Sequences
        Release 5.4

Results file us-09-910-186a-16.res made by bobryen on Thu 7 Nov 102 14:34:47-PST.

Query sequence being compared:US-09-910-186A-16 (1-432)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

Results of the initial comparison of US-09-910-186A-16 (1-432) with:
        File : US0812397S5A.pep
```

```
100-
    |
    |
 N  |
 U 50-
 M  |
 B  |
 E  |
 R  |
    |
    |
 O  |
 F 10-
    |
 S  |
 E  5-
 Q  |
 U  |
 E  |
 N  |
 C  |
 E  |
 S  0-----|----|----|----|----|----|----|----|----|----|----|----|----*----|
         |    |    |    |    |    |    |    |    |    |  **    **   |    |
 SCORE  0|  23|  46|  69|  92| 116| 139| 162| 185| 208|
 STDEV -7|  -6|  -5|  -4|  -3|  -2|  -1|   0|   1|
```

```
                        PARAMETERS
Similarity matrix     PAM-150     K-tuple                 1
Threshold level of sim.  16%      Joining penalty        20
Mismatch penalty          1       Window size           432
Gap penalty             5.00
Gap size penalty        0.05
Cutoff score              1
Randomization group       0

                 SEARCH STATISTICS
                 Mean    Median     Standard Deviation
Scores:          181      165           23.64

                 CPU               Total Elapsed
Times:        00:00:00.00          00:00:00.00

Number of residues:              1704
Number of sequences searched:       3
Number of scores above cutoff:      3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                                                Init.  Opt.
Sequence Name    Description                                           Length  Score  Score  Sig. Frame
--------------   -----------                                           ------  -----  -----  ---- -----
                                 **** 1 standard deviation above mean ****
1. US-08-123-975A-2 Sequence 2, Application U   850    208    264    1.14    0
                                 **** 0 standard deviation from mean ****
2. US-08-123-975A-3 Sequence 3, Application U   415    171    296   -0.42    0
3. US-08-123-975A-5 Sequence 5, Application U   439    164    256   -0.72    0
```

```
1. US-09-910-186A-16 (1-432)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =    208    Optimized Score    =   264    Significance   =   1.14
Residue Identity =    35%    Matches            =   163    Mismatches     =   231
Gaps             =    28     Conservative Substitutions    =               33

                 X        10        20        30        40        50
               MSYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVY
               ||||  ||| ||||||  : | || |||||||: :: :::  | |||| : |
AEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVE
380       390       400       410       420       430       440       450

          60        70        80        90       100       110       120
IYSTNRNQFGIYSSKPSEVNIAQNDIIYNGRYQNFSISFWVRIPKYFNKV---NLNNEYTIIDCIRNNNSG
|||:|||:|| || :  : | :| :|  || : :||||||||| :||||||   :|| ||| ||:| |||
L--NDKNQFKLTSSANSKIRVTQNONIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMK-NNSG
460       470       480       490       500       510       520

         130       140       150       160       170       180       190
WKISLNYNKIIWTLQDTAGNNQKLVFNTQMISISDYINKWIFVTINNRLGNSRIIYINGNLIDEKSISNLG
|||:| ||||||| |  |   ||  |||  |||:||||||||||||||| |:||||| |: |||||||  |
WKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFVTITNN-LNNAKIYINGKLESNTDIKDIR
530       540       550       560       570       580       590

         200       210       220       230       240       250       260
DIHVSDNILFKIVGCND-TRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYLLNLL
:: :|:||| | | | |  |:||||||:|||  || || |||| : :| : |||||||| |:|||  : | :
EVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYMFNAG
600       610       620       630       640       650       660

         270       280       290       300       310       320       330
RTDKSITQNSNF-LNINQQRGVYQKPNIFSNTRLYTGVEVIIRKKNGSTDISNTDNFVRKNDLAYINVVDRDV
   ||:| ||    :| ||  || ||||| |:|| | | |||||: |||||| |||| ||| |  |
NKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ
670       680       690       700       710       720       730

         340       350       360       370       380       390
EYRLYADISIAKPEKIIKLIRTSNSNSLGQIVMD-----SIGNNCTMNFQNNNGGNIGLLGFH------
|| | | | | |   :  | |:|  ||  |  | |     ||: | |  | :||||  | : ||
EWRVYTYKYFKKEEEKLFLAPISDSDEEYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI
740       750       760       770       780       790       800

         400       410        420
-----SNNLVASSWYYNNIRKN--TSSNGCFWSFISKEHGWQEN
     | | :::||  |: ||    ||:  || | :|||||
VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
810       820       830       840       850
```

```
2. US-09-910-186A-16 (1-432)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =    171    Optimized Score    =   296    Significance   =  -0.42
Residue Identity =    49%    Matches            =   205    Mismatches     =   168
Gaps             =    17     Conservative Substitutions    =               27

          10        20        30        40        50        60        70        80
LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKPSEVNIAQNNDI
             ||||||||||||||||||||||||||||||||||||||:||||||||||:|||||||| ::
RYESNHLIDLSRYASKINIGSKVNFPDIDKNQIQLFNLESSKIEVILKNAIV
X         10        20        30        40        50
```

```
        280       290       300       310       320       330       340
        360       370       380       390       400       410
RTSNSNNSLGQIIVMD------SIGNNCTMNFQNNNGGNIGLLGFH----------SNNLVASSWYYNNIR
                                                        |||  ||
PISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVK
        350       360       370       380       390       400       410

        420       430
KN--TSSNGCFWSFISKEHGWQEN
 :  ||:||:||:||  ::||  |
RKPYNLKLGCNWQFIPKDEGWTE
        420       430
                       X
```

```
         90       100       110       120       130       140       150
YNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQM
||| || || |||||||||||  :|||||||||  ||||||||| :||||||
YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQM
         60        70        80        90       100       110       120

        160       170       180       190       200       210       220
ISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIVGCNDT-RYVGIRYFKVFD
||||||||:|||||| :||  |:|||| || |:|| ||||:  | :|||||  :||  | ||:||||||
INISDYINRWIFVTITNNRLNNSKIYINGRLIIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFD
        130       140       150       160       170       180       190

        230       240       250       260       270       280       290
TELGKTEIETLYSDEDPSILKDFWGNYILLYNKRYYLLNLLRTDKSITQNS---NFLNINQQRGVYQKPNI
 ||| || | | :||||||||||  || |||||||||| ||||:|  |
KELNEKEIKDLYDNQSGILKDFWGDYLQYDKPYYMLNLYDPNKYDVNNVGIRGYMYLKGPRGSVMTTNI
        200       210       220       230       240       250       260

        300       310       320       330       340       350       360
FSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSNNS
 : || | |  :|| | ||| ||
YLNSSLYRGTKFIIKKYAS---GNKDNIVRNNDRVYINVVKNKEYRLATNASQAGVEKILSALEIPDVGNL
        270       280       290       300       310       320       330

        370       380       390       400       410       420
LGQIIVM----DSIGNNCTMNFQNNNGGNIGLLGFHS----NNLVASSWYYNNIRKNTSSNGCFWSFISKEH
 :  :    || | | | |                   :
SQVVVMKSKNDQGITNKCKMNLQDNNGNDIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDD
        340       350       360       370       380       390       400

430 X
GWQEN
|||
GWGERPL
410 X
```

3. US-09-910-186A-16 (1-432)
    US-08-123-975A-5 Sequence 5, Application US/08123975A

```
Initial Score    =    164    Optimized Score    =    256    Significance = -0.72
Residue Identity =    35%    Matches            =    358    Mismatches   =    226
Gaps             =    28     Conservative Substitutions =   156              33
```

```
         10     X   20        30        40        50        60        70
MSYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKPSEVN
                  |||  :  |:|: :|| ||
                FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVEL--NDKNQFKITSSANSKIR
         X      10        20        30        40        50

         80        90       100       110       120       130       140
IAQNNDIIYNGRYQNFSISFWVRIPKYFNKV--NLNNEYTIIDCIRNNNSGWKISLNYNKIIWTLQDTAGN
|| | : ||||||||  |||||||  | ||||||| : :|||||  | | |||||||||||
VTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMK-NNSGWKISIRGNRIIWTLIDINGK
        60        70        80        90       100       110       120

        150       160       170       180       190       200       210
NQKLVFNYTQMSISDYINKWIFWIFVTTNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIVGCND-TR
 |  | | ||||||| |||||| :||||||  | |:|| |:||||  || |  ::|||| ||
TKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQ
        130       140       150       160       170       180       190       200

        220       230       240       250       260       270       280
YVGIRYFKVFDTELGKTEIETLYSDEDPSILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNF-LNINQQR
 : :|| |  |  | |  |||||||||||||  ||||| ||||||||||| :|||| ||: |  |:||||
FIWMKYFSIFNTELSQSNIERYKIQSYSEYLKDFWGNPLMYNKEYYHFNAGNKNSYIKLKDSPVGEILTR
        210       220       230       240       250       260       270

        290       300       310       320       330       340       350
GVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLI
:: ||| : |  | |:  |  :|  ||  :| |  ||
SKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFPNLNQEMRVVTYKYFKKEEKLFLA
        280       290       300       310       320       330       340       350
```

```
OIV
OIIO  IntelliGenetics
OIV

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-17.res made by bobryen on Thu 7 Nov 102 14:45:51-PST.

Query sequence being compared:US-09-910-186A-17 (1-1368)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

        Results of the initial comparison of US-09-910-186A-17 (1-1368) with:
          File :US08123975A.seq
```

```
100-

N  -
U 50-
M  -
B  -
E  -
R  -

O  -
F 10-

S  -
E  5-
Q  -
U  -
E  -
N  -
C  -                                                *
E  -
S  0----|----|----|----|----|----|----|----|----|----|----|----|----|
                                                              |--|  566
SCORE 0   63  126  189  252  314  377  440  503    0            1
STDEV     -9   -8   -7   -6   -5   -4   -3   -2   -1    0

                    PARAMETERS

Similarity matrix    Unitary    K-tuple               4
Mismatch penalty     1          Joining penalty      30
Gap penalty          5.00       Window size         500
Gap size penalty     0.33
Cutoff score         1
Randomization group  0

                 SEARCH STATISTICS

Scores:        Mean        Median        Standard Deviation
               520         499           39.26

Times:           CPU                Total Elapsed
               00:00:00.00          00:00:00.00

Number of residues:              4027
Number of sequences searched:       3
Number of scores above cutoff:      3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                              Init.  Opt.
Sequence Name    Description                        Length  Score  Score  Sig.  Frame
-----------      -----------                        ------  -----  -----  ----  -----
                 **** 1 standard deviation above mean ****
1. US-08-123-975A-6 Sequence 6, Application U  1351   566    797    1.17    0
                 **** 0 standard deviation from mean ****
2. US-08-123-975A-4 Sequence 4, Application U  1338   498    706   -0.56    0
3. US-08-123-975A-1 Sequence 1, Application U  1338   498    706   -0.56    0

1. US-09-910-186A-17 (1-1368)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score      =   566    Optimized Score =   797   Significance =  1.17
Residue Identity   =   61%    Matches         =   829   Mismatches   =  488
Gaps               =   39     Conservative Substitutions =  0

                  20        30        40        50        60        70        80
     TGAAGGACACCATCCTGATCCAGGTCTTCAACAACTACATCTCCAACATCTCCAACGCCATCCTGTCCC
                       ||||||||||| ||| |||||| |||||||| ||||||| |||||| ||
                 ATGGCTTTCAACAACAAATACAATCCTGAACAACAATATCATCCTGAACC
                          X           10        20        30        40        50

           90       100       110       120       130       140       150
     TGTCCTACCGTGGTGGTCGTCTGATCGACTCTCCGGTTACGGAGCCACCATGAACGTCGGTTCCGACGTCA
        |||  |  ||||  |||||||||| |||||| |  |||||| ||  ||||| | ||  ||||||
     TGCGGTTACAAAGACAACAATCTGATCGGTCTGGTTACGGTGCTAAAGTGAAGTATACGACGGTGTTG
        60        70        80        90       100       110       120

          160       170       180       190       200       210       220
     TCTTCAAGCACATCGGTAACGGTCAGTTCAAGCTGAACAACTCCGAGAACTCCAACATCACCGCCCACCAGT
         |  |||      |||  ||  ||||||| ||||||| |||||||||| |||||||| |||| |
     AACTGAATGAC------AAGAACCAGTTCAAACTGACCTCTTCGCGCTAACTCTAAGATCCGTGTTACTCAGA
         130             140       150       160       170       180       190

          230       240       250       260       270       280       290
     CCAAGTTCGTCGTCTACGACTCCATGTTCGACAACTTCCATCAACTTCTGGTCCGTACCCCAAAGTACA
        |  ||| | ||| |||||||| ||| |||||||| ||||| |||||||| |||||||||||
     ATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTCTTCCTTCTGGATCCGTATCCCGAAATACA
        200       210       220       230       240       250       260

     300       310       320       330       340       350       360       370
     ACAACAACGACATCCAGACTCACCTGCGAGAACGAGTACCACCATCATCCTGTATCCAAGAACGACTCCGGTT
        |||| |||||||||||| ||||| |||||||||||||| ||||| ||||||| |||||||||||||||||
     AGAACGACGGTATCCCAGAATTACATCCACAATGAATACACCACCATCATCAACTGCATGAAGAATAACTCTGGTT
        270       280       290       300       310       320       330

            380       390       400       410       420       430       440
     GGAAGGTCTTCATCAAGGAGAAACCGTATCATCTGGACCGTGACGTCAACGCGCCAAGTCCAAGTCCATCT
        |  |||||||||| |||||||| ||||||||| |||||||| ||| || ||||||| |||| ||||
     GGAAGATCTTCATCCCGCGTAACCGTATCATCTGGACTGTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTAT
        340       350       360       370       380       390       400

        450       460       470       480       490       500       510
     TCTTCGAGTACTCCATCAAGGACACCAACTCCGACTCACTCACAACAAGTGGTTCTCCATCACCATCACCAACG
        ||||||||| ||||  |||||  ||| |||||||| | |||| ||||| ||||||| ||||||||| |||
     TCTTCGAATACAACATCCGTGAAGACATCTCTGAATATCACCATCAATCAACGGTGGTTCTTCGTTACCATCACCAACATA
        410       420       430       440       450       460       470

        520       530       540       550       560       570       580
     ACCGGTCGTGGGTAACGCCAACATCTACACATCAACACGGTTCCCTGAA---GAAGTCCGAGAAGATCCTGAACCTGG
        ||||||||| |||  ||||| | |||||||| ||| |  | |||| ||  ||||| | | ||||||
     AC---CTGACAATGCTAAAAATCTACATCAACACGGTAAACTGGAATCGTAAACTGGAATCTATAACCGACATCAAAGACATCCGTG
        480       490       500       510       520       530       540

        590       600       610       620       630       640       650
     ACCGTATCAACTCCTCCAACGACATCAGACTTCAAGCTGATCAACTGTACCGACAACTGGACCCAAGTTCGTCTGGA
        ||| || ||||| || |||||| ||||| |||||| |||||||| || |||||| ||||||| ||||| ||||||
     AAGTTAT---CGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACGTCAACGGTGACATCGATCGTGTTCATCCTGGA
        550       560       570       580       590       600       610

        660       670       680       690       700       710       720
     TCAAGGACTTCAACATCTTCGGTGTGGAGTCGAGACGCCACCGAGGTCTCCTCCCTGTACTGACTGATCCAGTCCT
```

```
          |  | |||||  |||||| |||         ||     |||  ||||||| ||||| ||||||||    |||||||||||
GAATTCACGATGAAGGACACCATCCTGATCCCAGGTCTTCAACAACTACCATCTCCTCCAAACGCC
CTCGAGCCATGGCTC--GTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCC
     X          10        20        30        40        50        60

                                                     80        90       100       110       120       130
          ||||| |||||    |||| |  ||||||| ||| ||||||  |||| ||||| |||||||  ||||||||  |||
ATCTGTCCCTGCGCTACCGTGGTGGTCGTCTGATCGACTCCTCCGGTTACGGAGCCACCATGAAGCGCGGT
|||||| || ||| | |||||||||||| |||||| |||||||||||||| |||||||||||||||||
ATCCTGAACCTGCGCTACCGTGGTGATGTCAACAAGAATACCATATGTTCAATGTTCAATCGGT
  70        80        90       100       110       120       130

                            150       160       170       180       190       200       210
TCCGACGTCATCTTCAACGACATGTACGG
TCTAAAGTTAACTTCGATCCGACGATCGACAAGAATCAGACTTCCAAATCGAA
 140       150       160       170       180       190       200
```

(The remainder of the page continues the aligned nucleotide sequences.)

```
GCCCACCAGTCCAAGTTGCTCGTCGTCTAGCGACTCCATGTTCGACAACTTCTCCATCAACTTCTGGGTCCGTACC
                     ||    ||  ||||||                |||  |  ||||||  ||||  ||||||||
                     GTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATC
        210      220      230      240      250      260      270      280

                                    ||  |||||  ||||  |  |  ||||||||||||||||||
CCAAAGTACAACAACAACGACCATCCAGATCCAGAGCTACCTGCAGAACGAGTACACCATCATCCTGTATCCAAGAAC
        290      300      310      320      330      340      350      360

                                   ||  ||  ||| |         |  ||||||| |  |  ||||||
CAAGAA---ATACGTCGTGTCTGGTAACAAGGACAATATGTTCGCAACAATGATCGTGTATACGATCAATCAAGTGT
        920      930      940      950      960      970      980

3.  US-09-910-186A-17 (1-1368)
    US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =    498     Optimized Score    =      706     Significance   =    -0.56
Residue Identity =     54%    Matches            =      758     Mismatches     =     551
Gaps             =     70     Conservative Substitutions                      =       0
```

```
 |  |      ||||   ||||    |  |      |    |  |   ||  ||         || ||    ||| || |||| ||
GCTCTGG----AAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGG
   1060         1070        1080        1090        1100        1110        1120

1140        1150        1160        1170        1180        1190        1200
GACCACCTACAACTGTCAGATCCTGTGCGAGAAGGACACCAAGACCTTCGGACTGTTCGGTATCGGTAAGTT
 | |||  ||| |||| | ||  | ||||||| |  | |||||| |||             |||| || ||
TATCACTAACAAATGCAAAA---TGAATCTGCAGGACAACAA-----------TGGTAACGATA----
   1130        1140        1150        1160                1170

1210        1220        1230        1240        1250        1260        1270        1280
CGTCAAGGACTACGGTTACGTCTGGGACACCTACGACAACTACTTCTGTATCTCCCAGTGGTACCTGCGTCG
 ||  | |||||||| ||||| | | |||   |  |  | | | ||| | | |||||||| | |||||
--TCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCAACTGGTACAAATCGTCA
   1180        1190        1200        1210        1220        1230        1240

1290        1300        1310        1320        1330        1340        1350
TATCTCCGAGAACATCAACAAGCTGCGTCTGGGATGTAACTGGCAGTTCATCCCAGTCGACGAGGGTTGGAC
 |||  ||| |   |  |   | ||||| ||  |  |||||||||||||| | | || |||||| ||||||
GATC-----GAACGT-TCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGG
   1250        1260        1270        1280        1290        1300

         X
       1360
CGAGTAATAGGAATTC
 ||    |
TGAACGTCCCCTGTAACCCGGGAAAGCTT
   1310    X 1330
```

```
> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-17-inv.res made by bobryen on Thu 7 Nov 102 14:46:08-PST.

Query sequence being compared:US-09-910-186A-17' (1-1368)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

Results of the initial comparison of US-09-910-186A-17' (1-1368) with:     complement
         File : US08123975A.seq
```

```
100-

N
U   50-
M
B
E
R

O
F   10-

S
E    5-
E
Q
U
E
N
C
E
S    0-----------------------------------
SCORE 0|   4   |8  |12  |16  |20  |24  |28| |32  |36
STDEV -4  -3   -2  -1   0   *   *   0  28| 32
                                                0
```

```
                  PARAMETERS

Similarity matrix    Unitary    K-tuple            4
Mismatch penalty     1          Joining penalty   30
Gap penalty          5.00       Window size      500
Gap size penalty     0.33
Cutoff score         1
Randomization group  0

            SEARCH STATISTICS

Scores:      Mean      Median     Standard Deviation
              32        25              6.93

Times:        CPU                  Total Elapsed
            00:00:00.00            00:00:00.00

Number of residues:           4027
Number of sequences searched:    3
Number of scores above cutoff:   3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
Sequence Name      Description                                          Length  Init.  Opt.   Sig.  Frame
                                                                                Score  Score  Score
-----------------  ---------------------------------------------------  ------  -----  -----  ----  -----
 1. US-08-123-975A-4  Sequence 4, Application U                          1338    36    464   0.58    0
 2. US-08-123-975A-1  Sequence 1, Application U                          1338    36    464   0.58    0
                      ****  1 standard deviation below mean ****         36          24
 3. US-08-123-975A-6  Sequence 6, Application U                          1351    24    52   -1.15    0
```

```
 1. US-09-910-186A-17' (1-1368)
    US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =    36    Optimized Score       =   464   Significance =    0.58
Residue Identity  =   40%    Matches               =   563   Mismatches   =    708
Gaps              =          108    Conservative Substitutions                =      0
```

```
             X         10        20        30        40        50
             GAATTC--CTATTACTCGGTCCAACCCTCGTCGACTGGGATGAACTGCCAGT
             |||||||  || ||| ||||||||||| || ||||  ||||||||||
GTCTGCTGCGTCTACCTTCACTGAATACATCAAGAACATCATCAACTCCCATCCTGAACCTGCGCTACGAAT
   20        30        X   40       50        60        70        80

                60        70        80        90       100       110
TACATC-CCAGACGCAGCT-TGTTGATGTTCTCGGAGATACGACGCAGGTACCCACTGGGAGAT----ACAGA
||| ||   ||||| ||||  |||| ||||| ||| ||||  ||||||| ||| |||||| |||    | |||
CCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGA
   90       100       110       120       130       140       150

               120       130       140       150       160       170       180
AGTAGTTGTCGTAGGTGTCCCACGACGTAACCCTAGTCCTTGACGAACTTACCGATACCGAACAGTCCGAAGG
|||||||| |||||||||||| ||| ||| || ||||||| |||| ||||  ||||| ||||||||| |||||
TCGACAAGAATCAGATCCAGCTGTGTTCAATCGGAATCTTCCAAAATCGAAGTTAATCCTGAAGAATGCTATCG
  160       170       180       190       200       210       220       230

              190       200       210       220       230       240       250       260
TCTTGGTGTCCTTCTCCCACAGGATCGTGACAGTTGAGGTGGTCTTCTCGTAGGTCGTATCCCGAAATAGTTCAACTCCATCT
|||||   |||| |||  || ||||   |  || |||||   ||||| |||| ||| |||||||||||| |||||||
TATACAACTCTATGTACGAAACTTCTCCACCTCGTTCTGATCCGTATCCGAGTACTTCTTGATCGTCGAGGA
  240       250       260       270       280       290       300

              270       280       290       300       310       320
CGTCGTAGAAGGTAGGTCGTCGTTGATTGGGGCCAGGAACAGCGTGGGTCTGGA---TCTCCTTGGAGT--
|||||  |||||  ||||| |||| ||||  ||||||||| |||||| ||||||   ||||| |||||
CTCTGAACAATGAATACACCATCAACTCACTCGCATGGAAACAATTCTGGTTGGAAAGTAGTATCTCTGAACTACG
  310       320       330       340       350       360       370

              330       340       350       360       370       380       390
TGACCAGGACGTAGACACGGTAGGACTCGTCGGAGACGTTCGGATGTTCGGATGTGATGGTAGATGAGTAGTCACCCTCAC
||||| ||||| |||  ||| ||||| ||||| ||||  |  || |  || |||||| || |||| |||||||||
GTGAAATCATCTGGACTCTGGACGTCTGCGAGGACACTCAGGAAT------CAAACAGCGTGTTGTTGTATTCAAATACTC
  380       390       400       410       420       430

              400       410       420       430       440       450       460
GGACGGATGTTGTCGTTGTTGATGTTACGGGAGTTGGAGG-CCTTCTTGATGATGAAACGGCAGACCCAGGTAC
|| | || |||| | |||| | ||  | |   |  |||| | |||||  ||  |||||  ||| ||| |||| ||
TCGAGATGACAACATCCTCGA--CTACACAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAAT
  440       450       460       470       480       490       500

              470       480       490       500       510       520       530       540
AGGTTCTGGTAGTTGATGGCGGCGGCCGTTGTTGAAGTTGGTACGAGGGGCGGCGTCTCACCCATGGAGGCCTTGGAG
||   |  |||| |  ||||||  ||  || |  | |   |  ||  |||   ||| ||  |||||  |||||||||
AACTCCAAAATCTACAATCAACGCGCCGTCTGA--TCGACCAGAAACCGATCTCCAATCCGGTAACATCCA-
  510       520       530       540       550       560       570

              550       560       570       580       590       600       610
AAGTACTTGATGTAGATGTTCGTTCGCATACCCTGGTTGAACAGGTACTGGGGTGTCGTAACGCAGTGGGTTT
||   ||| || | ||||  |||| ||  | |  | || || || |     ||||  ||
------------CGCTTCTAATAACATCATGTTCAAACTGG----ACGGTTGTCGTCGACACTCACCCGCTA
  580       590       600       610       620       630

              620       630       640       650       660       670       680
CCCCAG---AAGTCCTTCAGGGTGTT-GGTGGGAGGACTGGATCCAGTACAGGGAGGAGGACCTTCGGCGTGCGT
| |||    ||||| |||  |  |||                      ||||| |  ||  ||| |||||
```

```
        GGTGCTGCTCTACCTTCACTGAATGAAATACATCAAGAACATCATCCATCCTCGAACCTGCGCTACGACAA
        |||||  ||||| |||| ||
    20      30      X 40       50      60      70      80

                                                 TACATC-CCAGACGCAGCT-TGTTGATGTCTCGGAGATACGACGCAGGTACCACTGGGAGAT----ACAGA
                                                 ||||  |||||| ||| ||||     |||||
    50      60      70      80      90      100     110

CCAATCACCTGATCGACCTGTCTCGCTACGCCTTCCAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGA
|||   |||| || ||| |     |||| ||||  |||||||||||  |||||||
   90      100     110     120     130     140     150

AGTAGTTGTCGTAGGTGTCCCAGACGTAACCGTAGTCCTTGACGAACTTACGGATACCGAACAGTCCGAAGG
    |||||||||||||| |||  |||||||     ||| ||||  |||| ||||||  |||| |||||
   120     130     140     150     160     170     180

TCGACAAGAATCAGATCCAGCTGTCAATCTCGAAATCTGGAATCGTTCTCAACTTCAACTCCAATCT
|||||||||||||||||||   ||||||   ||||||||||  |||||||  ||||||||||   |||
   160     170     180     190     200     210     220     230

TCTTGGTCCTTCTCGCACAGGATCGACAGTTGACAGTTGAGGTGGTCTTCTCGTAGTACTTCTTGATCTGCAGGA
||| || ||||||| ||||||||  |||||||||||||||| |||||  |||| ||||||||  |||
   190     200     210     220     230     240     250     260

TATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCGAAATACTTCAACTCCATCT
|||||| || ||||  |||||  ||||||| ||||||||||||||||  |||||||  ||||||||
   240     250     260     270     280     290     300

CGTCGTAGAAGGTAGGTCGTCGTTGATTGGGGGCCAGGACAGCTGGGTCTCGGA---TCTCCTTGGAGT---
|||||  ||||||||||||||||||||  |||||||||||||||||||||||||     ||||||  |||
   270     280     290     300     310     320

CTCTGACAATGAATACACCATCCATCAACTGCATGGAAACAATTCTGGTTGGAAAGTATCTCTGAACTACG
| |||||||||  |||||  ||||||||||||||  |||||||||||||| ||| |||||||||||| |||
   310     320     330     340     350     360     370

TGACCAGGACGTAGACACGGTAGGACTCGTCGGAGAGTGTTGTCGATGGTCAGGATGAGTAGTCACCCCAC
||||||||||||||| ||||||| |||| ||||||||||||||||||||||  |||| ||||||| |||||
   330     340     350     360     370     380     390

GTGAAATCATCTGGACTCTGAGGACACTCAGGAAAT------CAAACAGCGTGTTGTTATTCAAATACTC
 |||||||||||||| ||||||||||||| ||||||      ||||||| ||||| |||||  ||||||
   380     390     400     410     420     430

GGACGAGTTGTCGTTGTGATGTTACGGGAGTTGGAGG-CCTTCTTGATGATGAAACGACGACCCAGGTAC
|||||||||||||| || |||||||||||||||| |||  |||||||||||||||||||||||||||||
   400     410     420     430     440     450     460

TCAGAGATGATCAACATCTCTGA--CTACAATCGCTGCTTGAAGTGGTGATCCATCACCAACAATCGTCTGGAAT
|||||||||| ||||||||||||    ||| |||||| |||||| |||  |||| |||| ||||||||||||||
   440     450     460     470     480     490     500

AACTCCAAAATCTACATCTGTTCGAGGACTGGTCTGA---TCGACCAGAAACCGATCTCCAATCTGGGTAACATCCA-
||||||| ||||||  ||||||||||||| |||||||     |||||||||| ||||| |||||||||||   |||||
   510     520     530     540     550     560     570

AAGTACTTGATGTAGATGTTCTGCATCCCGTTGACATCAGTAGTACGGGTGTGTCGGTGTACTGGCACTCCACCGTA
|||||||||||| ||| ||||| ||||||| ||||||||||| |||||| ||||| |||||||||  ||||||||||
   550     560     570     580     590     600     610

--------CGCTTCTAATAACATCAATGTTCAAACTGG------ACGGTTGCGTGCACTGCTTCACCGCTA
        |||||||||||||||||||||||| ||||        |||||||||||  ||||||||||||
   580     590     600     610     620     630

CCCCAG---AAGTCCTTCAGGGTGTT-GGTGGGAGGACTGGATCGGATCCAGTACAGGAGGACCTCGGGTGTGGCGT
|| |||   ||||||||||||||||   ||||||||||||||| ||||||||||||||| ||||| ||||| |||
   620     630     640     650     660     670     680

CATCTGGATCAAATACTTCAATCTGTTCGACAAAGACTGAACTGAACAAAGAAATCAAAGACCCTGTACGACAA
||||   || |||||||||||||||||| |||||||||||||||||||||||||||| ||||||||||||||||
   640     650     660     670     680     690     700

TCTACGACGACCGAAGATGTTGAACTGCCTTGATCCAGCAGCGAACTTGGCGGTACGCAGTGTCGGTTGATCAGCT
||||||||||||||||||||||||||||||||||||||||  |||||||||| |||||||||||||| |||||||
   690     700     710     720     730     740     750

CCAGTCCAATTCTGGTATCCTGAAAGACTT-----CTGGGGTGACTACCTGCAGTACGACAAAC
|||| |||||||| ||||  ||||||| |||     |||||| |||||||||||||||  ||||
   710     720     730     740     750     760

CGTACTACAT------GCTGAATCGTACGATCCGACAAATACGTTCAGGTGTCAACAATGTAGGTATCCGC
||||||       |||||||  ||||||||| |||||||||||||||  ||| || |||||  |||||||
   770     780     790     800     810     820

TGAGTGTAGATGTTGGCGTTACCGACACGGTCGTTGGTGATGGTGAGGAGACCACTTG-----TTGATGT
 |  ||||||| ||||||| |||||| ||||||||||||||||||||||||  ||||      ||||||
   830     840     850     860     870     880     890
```

```
CATCTGGATCAAATACTTCAATCTGTTCGACAAGAACTGAACGAAAGAAAATCAAAGACCTGTACGACAA
                                                   640     650  ...
```

```
2. US-09-910-186A-17' (1-1368)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    = 36      Optimized Score = 464    Significance = 0.58
Residue Identity = 40%     Matches         = 563    Mismatches   = 708
Gaps             = 108     Conservative Substitutions = 0

   X        10       20        30        40       50
GAATTC--CTATTACTCGGTCCAACCCTCGTCGACTGGGATGATGAACTGCCAGT
```

```
GG--TTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGT
  830     840     850     860     870     880     890

AGTCGGAGATGTTGTCCTTGGATGAGTACTTCGAAGAGAAGATGGGACTTGGAC-TTGGCGTTGACGTCGATCAGG
  900     910     920     930     940     950     960
ACCGTGGTACCCAAAATTCATCATCAAGAAATACCGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATC
  900     910     920     930     940     950     960

GTCCCAGATGATACGGTTCCCTTGATGGAGGAGACCTTCCAACCGGAGTCGTTCTTGATACGAGGAGGATGATGGTG
  970     980     990     1000    1010    1020    1030
GTGTATACATCAATGTT---GTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTG
970     980     990     1000    1010    1020    1030

TACTCGTTCTGCAGGTAGGTCGGATGCGTCGTTGTTGTT-GTACTTGGGGTACGGACCCAGAAGTTGCATGGA
  1040    1050    1060    1070    1080    1090    1100
TAGRAAAAGATCTTGTCTGCTGGAAATCCGGACGTTGGTAATCGTCTCAGGTAGTTGTAATGAAATCCA
1040    1050    1060    1070    1080    1090    1100    1110

GAAGTTGTCGAACATGGAGTCGTAGACGA---CGAACTTGGACTGGTGGCGGTGATGTTGGAGTTCTCGGA
  1110    1120    1130    1140    1150    1160    1170
AGA----ACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGG-
1120    1130    1140    1150    1160    1170

GTTGTTCAGCTTGAACTGGCTACCGTTACCGATGTCGTTGAAGATGACGTCCGAACGACGTTCATGGTGGCTCC
  1180    1190    1200    1210    1220    1230    1240
TTTCATCGGTTTCCAC--CAGTTCAACAATATCGCTAAACTGGTTG--------CTTCCAACTGGTACA
1180    1190    1200    1210    1220    1230

GTAACCCGGAGGAGTCGATCAGAGACGACCACCACGGTAGGAC-AGGGACAGGATGGCGTTGGAGGAATCGTTGG
  1250    1260    1270    1280    1290    1300    1310
ATCGTCAGATCGAACGTTCCTCCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGA-CGGTTGG
1240    1250    1260    1270    1280    1290    1300

AGATGTAGTTGTTGAAGAACCTGGATCAGGATGGTGTCCTTCATCGTGAATT
  1320    1330    1340    1350    1360
GGTGAACGTCCGCTGTAACCCGGGAAAGCTT
1310    1320    1330              X
```

3. US-09-910-186A-17' (1-1368)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

```
Initial Score    =  24      Optimized Score       =  52      Significance =  -1.15
Residue Identity =  42%     Matches               =  68      Mismatches   =  81
Gaps             =  10      Conservative Substitutions =  0
```

```
           X       10        20        30        40        50
           GAATTCCTATTACTCGGTCCAACCCTCGTCGACTGGGATGAACTGCCAGTTA
           ||      |      ||  ||  |||  ||   |||  |||    |||||||
GAATCTGGTATCGTATTCGAAGAATACAAAGACTACTTC--TGCATCCAAATGGTACCTGAAGGAAGTTA
1190    1200    X       1210    1220    1230    1240    1250

    60        70        80        90        100       110       120
CATCCCAGACGCCAGCTTGTTGTGATGTTCTCGGAGATACGACGCAGGTACCACTGGGAGATAACAGAAGTAGTTG
   |||     |     ||  ||   ||||||| |||     |||||  |||||||   ||
AACGCAAACCCGTACAACCTGAA---ACTGGTTGCAATTGGCAGTT--CATCCCGAAAGACGAAGGTTG--G
1260    1270    1280    1290    1300    1310

      130       140       150       X       170
TCGTAGGTGTCCCAGACGTAACCGTAACCGTAGTCCTTGACGAACTTACCGATACCGAACA
   ||        |||   |  |||   ||     ||  ||||   |||
ACCGAATAGTAACCTCTAGAGTCG-AGGCCTGCAG
1320    1330    1340    1350
```

```
> O <
O| |O   IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-18.res made by bobryen on Thu 7 Nov 102 14:35:06-PST.

Query sequence being compared:US-09-910-186A-18 (1-449)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-18 (1-449) with:
         File :US08123975A.pep

```
100-
    -
    -
 N  -
 U 50-
 M  -
 B  -
 E  -
 R  -
    -
 O  -
 F 10-
    -
    -
 S  -
 E  5-
 Q  -
 U  -
 E  -
 N  -
 C  -
 E  -
 S  0-|----|----|----|----|----|----|----|----|----|----|----|
SCORE  0   23   46   69   92  115  138  161  184  207
STDEV                                             *            207
                                                              -9
```

PARAMETERS

```
Similarity matrix    PAM-150         K-tuple                      1
Threshold level of sim. 16%
Mismatch penalty       1             Joining penalty             20
Gap penalty          5.00            Window size                432
Gap size penalty     0.05
Cutoff score           1
Randomization group    0
```

SEARCH STATISTICS

```
                Mean      Median       Standard Deviation
Scores:          206        207            0.58

                 CPU                      Total Elapsed
Times:       00:00:00.00                  00:00:00.00
```

Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
                                                                        Init. Opt.
Sequence Name    Description                          Length Score Score Sig. Frame
-------------    -----------                          ------ ----- ----- ---- -----
                               ****   1 standard deviation above mean ****
 1. US-08-123-975A-5 Sequence 5, Application U     439   319   319  1.73    0
 2. US-08-123-975A-2 Sequence 2, Application U     850   207   326  1.73    0
                               ****   0 standard deviation from mean ****
 3. US-08-123-975A-3 Sequence 3, Application U     415   206   262  0.00    0
```

```
1. US-09-910-186A-18 (1-449)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score     =  319    Optimized Score  =  319    Significance =  1.73
Residue Identity  =  49%    Matches          =  220    Mismatches   =  182
Gaps              =   9     Conservative Substitutions =  33
```

```
           10        20        30        40        50        60        70
MKDTILIQVFNNYISNISSNAILSLSYRGGRLIDSSGYGATMNVGSDVIFNDIGNGQFKLNNSENSNITTAHQ
||||||:|| ||| :|| :|||||||||||||||||||||||||||||||||||||||| ||:::: :|::||
         FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELND--KNQFKLTSSANSKIRVTQ
  X              10        20        30        40        50        60

          80        90       100       110       120       130       140
SKFVVYDSMFDNFSINFWVRFPKYNNNDIQTYLQNEYTIISCIKNDSGWKVSIKGNRRIWTLIDVNAKSKSI
::: ||::| |::|| :::| :|:|:||::||:|||::||:||:|:|||:|:|||:||||||||||:::: ::|
NQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV
  70              80        90       100       110       120       130

         150       160       170       180       190       200       210
FFEYSIKDNISDYINKWFSITITNDRLGNANIYINGSLKKSEKILNLDRINSSNDIDFKLINCTDTTKFVWI
||||::|:::| ::|||::|||||:|| | :|| ::|    :|:| :| |:|||:|:|:|:||||:||:::::|:
FFEYNIREDISEYINRWFFVIITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWM
 140             150       160       170       180       190       200

         220       230       240       250       260       270       280
KDENIFGRELNATEVSLYWIQSSTNTLKDFWGNPLRYDTQYYLFNQGMQNIYIKYFSKASMGETAPRTNFN
|||:|::::|||||||||||:::::::||||||||||||||||||||||||||||:::|:|||::|::||||||
KYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN
 210             220       230       240       250       260       270

         290       300       310       320       330       340       350
NAA--INVQNLYILGLRFIIKKASNSRNINNDNIVREGDYIILNIDNISDESYRVVLVNSKEIQTQLFLAPI
:||    :|:|:|||:|::|||||:|:|:| :|| ::|:|:||| ||||| :||::|:|:|:|||:|||||||||
QNSKYINYRDLVIGEKFIIRRKSNSQSI-NDDIVRKEDYILDFNLNQE-WRVYTYKYFKKEEEKLFLAPI
 280             290       300       310       320       330       340

         360       370       380       390       400       410       420
NDDPTFYDVLQIKKYYEKTTYNCQILCEKDTKTFGLFGIGKFVKDY--GYVWDTYDNYFCISQWVLRRISEN
:|||:|| :|:|:|||||:| : ||:||:| ||||:|||||||||||||||:|||||:| :|| :|||| :: :|
SDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGHRFYESGIVFEEYKDYFCISKWYLKEVKRX
 350             360       370       380       390       400       410

         430       440
INKLRLGCNWQFIPVDEGWTE                  X
|:||:|||||||||:|:|||||
PYNLKLGCNWQFIPKDEGWTE
 420             430
```

```
2. US-09-910-186A-18 (1-449)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score     =  207    Optimized Score  =  326    Significance =  1.73
Residue Identity  =  49%    Matches          =  225    Mismatches   =  186
Gaps              =   9     Conservative Substitutions =  33
```

```
           10        20        30        40        50
EKSKVNKYLKTIMPFDLSIYTNDTILLEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELND
                  ||:||| :|||::||:|||::|||||||||||||||||||||||||||||||||||
                  MKDTILIQVFNNYISNISSNAILSLSYRGGRLIDSSGYGATMNVGSDVIFND
  X              X         10        20        30        40        50
 390             400 X    410       420       430       440       450
```

```
            270       280       290       300       310       320       330
            370       380       390       400       410       420       430
DVLQIKKYYEKTTYNCQILCEKDTKIFGLFGIGKFVKDYGYVWDTYDNYFCISQWYLRRISENINKLRLGCN
:|||||||||||| ||: ||  |  ||||||||||||||:  |:||||||||||||||||||||||||||| |||
QVVVMKSKNDQGITNKCKMNLQDNN------GNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRT--LGCS
            340       350       360             370       380       390       400

440       X
WQFIPVDEGWTE
:||||||:||
WEFIPVDDGWGERPL
            410 X
```

```
            60        70        80        90        100       110       120
IGNGQFKLNNSENSNITAHQSKFVVYDSMFDNFSINFWVRTPKYNNNDIQTYLQNEYTIISCIKNDSGWKVS
|:||:||| || ::|: |:|||| :||:: ||||:|:|:|:||:: | |||:|||||||:|:|:|::||||:|
--KNQFLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKKNNSGWKIS
            460       470       480       490       500       510       520

            130       140       150       160       170       180       190
IKGNRIIWTLIDVNAKSKSIFFEYSIKDNISDYINKWFSITTNDRLGNANIYINGSLKKSEKILNLDRINS
|:||||||||:||:| ||:|||||:|:||:|||||:||:::| || ||||||||||:|:|| :| |||:: :
IRGNRIIWTLLIDINGKTKSVFFEYNIREDISEYINRWFVTIINN-LNNAKIYINGKLESNTDIKDIREVIA
            530       540       550       560       570       580       590

            200       210       220       230       240       250       260
SNDIDFKLINCTDTTKFWIKDFNIFGRELNATEVSSLYWIQSSTNTLKDFWGNPLRYDTQYYLFNQGMQNI
 | | |||:| :|  :|:| ||| |:: |  :|||:: |::| ::|||||||||| :::||:| ||  ::|:
NGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNS
            600       610       620       630       640       650       660

            270       280       290       300       310       320       330
YIKYFSKASMGETAPRTNFNNAA--INYQNLYLGLRFIIKKASNSRNINNDNIVREGDYIYLNIDNISDESY
||| :  :|  ||  :|   |:|   |||: ||:|: |||::|||| ||: || |||:|||||: :||:|: |
YIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSI-NDDIVRKEDYIYLDFFNLNQE-W
            670       680       690       700       710       720       730

            340       350       360       370       380       390       400
RVYVLVNSKEIQTQLFLAPINDDPTFYDVLQIKKYYEKTTYNCQILCEKDTKTFGLFGIGKFVKDY--GYVW
|||  :  |||  :|||||| :|  :||  ||::|:|    | |:| :|| :: |  ||:::||||   ||
RVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPFYSCQLLFKDEESTDEICLGIHRFYESGIVF
            740       750       760       770       780       790       800

            410       420       430       440       X
DTYDNYFCISQWYLRRISENINKLRLGCNWQFIPVDEGWTE
 :|||||||:|||:: :::|| ||||||||||||:|||||||
EEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
            810       820       830       840       850
```

3. US-09-910-186a-18 (1-449)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

```
Initial Score    =    206    Optimized Score   =    262    Significance  =   0.00
Residue Identity =    35%    Matches           =    151    Mismatches    =    232
Gaps             =     12    Conservative Substitutions =    29
```

```
            10        20      X 30        40        50        60        70
LIQVFNNYISNISNAILSLSYRGGRLIDSSGYGATMNVGSDVIFNDIGNGQFKLNNSENSNITAHQSKFVV
                 |:: |::|||||| :|  : ||:| :|::| |:: |  |::|| |||:||::| :||
RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
          X 10        20        30        40        50

            80        90        100       110       120       130       140
YDSMFDNFSINFWVRTPKYNNNDIQTYLQNEYTIISCIKNDSGWKVSIKGNRIIWTLIDVNAKSKSIFFEYS
|:||::|||:||||:|:|||:|  |:|||:||||| | :|:||||||||:||:|||||:|  ::|::|: |:
YNSMYENFSTSFWIRIPKYFNS---ISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYS
            60        70        80        90        100       110       120

            150       160       170       180       190       200       210
IKDNISDYINKWFSITTNDRLGNANIYINGSLKKSEKILNLDRINSSNDIDFKLINCTDTTKFVWIKDFNI
|::|||||||:|::: |||:|  :||||||| ||  | : | |  |  || :|||:|    ::| |||| ||
QMINISDYINRWIFVIITNNRLNNSKIYINGRLIIDQKPISNLGNTIHASNNIMFKLDGCRDTHRYIWIKYFNL
            130       140       150       160       170       180       190

            220       230       240       250       260       270       280
FGRELNATEVSSLYWIQSSTNTLKDFWGNPLRYDTQYYLFNQGMQNIYIKYFSKASMGETAPRTNFNNAAIN
|::|||::|::  |  |: :| ||||||   ||  |:: |:   ::  |::|:   ::|  :   | :  |
FDKELNEKEIKDLYDNQSNSGLLKDFWGDYDLQYDKRPYYMLNLYDDPNKYFYDVNNYGIRGYMYLKGPRGSVMTT
            200       210       220       230       240       250       260

            290       300       310       320       330       340       350
YQNLYLGLRFIIKKASNSRNINNDNIVREGDYIYLNIDNISDESYRVYVLVNSKEIQTQLFLAPINDDPTFY
  | | |  |||||:|:| :: :|:|:||: | |:| :| :|    : | : :|||   ::| | ||: :
NIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLS
            300       310       320       330       340       350       360
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-19.res made by bobryen on Thu 7 Nov 102 14:46:34-PST.

Query sequence being compared:US-09-910-186A-19 (1-1242)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-19 (1-1242) with:
File : US08123975A.seq

```
                                                           Init. Opt.
Sequence Name    Description                    Length Score Score Sig. Frame
--------------   -----------                    ------ ----- ----- ---- -----
 1. US-08-123-975A-4 Sequence 4, Application U   1338   110   448  0.63   0
 2. US-08-123-975A-1 Sequence 1, Application U   1338   110   448  0.63   0
                  **** 1 standard deviation below mean ****
 3. US-08-123-975A-6 Sequence 6, Application U   1351    99   477 -1.10   0
```

1. US-09-910-186A-19 (1-1242)
US-08-123-975A-4 Sequence 4, Application US/08123975A

```
Initial Score   =  110    Optimized Score        =  448   Significance =  0.63
Residue Identity =  43%   Matches                =  546   Mismatches   =  580
                          Conservative Substitutions = 133 Gaps        =    0
```

```
                    X        10        20        30        40        50
              ATGGCTCTGAA--CGACCTGCATCAAAGTTAACAAACTGGGACCTGTTCTT
CCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTT--AACTTCGATCCGATCGA
 100        110   X  120       130       140       150       160

CTCCCCGTCTGAAGACAACTTCACTAACGACCTGAACAAAGGCGAAGAAATCACCTCCGACACTAACAT--
CAAGAATCAGATCCCAGCTGTTCAATCTGGAATCTTCAAATCGAAGTTATCCTGAAGAATGCTATCGTATA
 170        180       190       200       210       220       230

CGAAGCTGCTGAAGAAACATCTC--------TCTGGA-CCTGATCCAGCAGTACTACCTGACTTTCAACTT
CAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCTTCACCTCCATCTCCCAAATACTTCAACTCTCT
 240        250       260       270       280       290       300

CGACAACGAA---CCGGAAAACATCCATCAACTGCATCGAAAACAATTCGGTGGAAAGTATCTCTGAACTACGGTGA
GAACAATGAATGCATCACCACCATCATCAACTGCATCGAAAACAATTCAAACTGGACAAATA----------CAC
 310        320       330       340       350       360       370

ACTGGATGCCGACATCGAACGCTCGCAGGACACTCAGGAAATCAAACACGCGTGTTGTATTCAAATACTCTCAGATGATCAA
AATCATCTGGACTCTGCGAGGACCTCAGGAAATCAGGAAATCAGGAGGCTACTGAAGCTGGTTCCTGGGTTGG--GTTGA
 380        390       400       410       420       430       440       450

CATGTTCCACTACT-----GGCTGCTCAGGAATTCGAACACGGTAATC-TCGTATCGGTCTGACTAACTC
CATCTCTGACTACATCAATCGGTCGTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTA
 460        470       480       490       500       510       520

CGTTAACGAAGCTCTGCTGAACCCGTCTCGGGCGTTAC-------ACCTTCTCTCTCTTCCGACTAC-----
CATCAACGGCGCCGTTGATCGACCGACCAGAAACCGATCTCCAAATCTGGGTAACATCCACGGCTTCTAATAACATCAT
 530        540       550       560       570       580       590

GTTCAAACTGGACGGTGTCGTGCACACTCACCGGTACATCACCGTGACACTGTGAAGCTGGTTCCTGGGTTGG--GTTGA
ACTGAACGAAAAGAAATCAAAGACCTGTACGACAACCAGTCAATTCTGTATCCTGAAAGACTTCTGGGG
 600        610       620       630       640       650       660

ACAGCTGGTTCACGACTTCACCGAC-----GAAACTTCTGAAGTTTCCACCACTGACAAAATCGCTGACCA
ACTGAACGAAAAGAAATCAAAGACCTGTACGACAACCAGTCAATTCTGTATCCTGAAAGACTTCTGGGG
 670        680       690       700       710       720       730

TCACTATCATCATCCCGTACATCGGCGCCCGGCTCTGAACATCGTGACATCGTGTAACAAGACGACTTCGT--
 550        560       570       580       590       600       610
```

```
 100-
     -
     -
     -
     -
  N  -
  U 50-
  M  -
  B  -
  E  -
  R  -
  O  -
  F 10-
     -
  S  -
  E 5-
  Q  -
  U  -
  E  -
  N  -
  C  -
  E  -
  S  0---------------------------------------------------
SCORE 0   12   24   37   49   61   73   86   98  110
STDEV    -9   -8   -7   -6   -5   -4   -3   -2   -1   0
```

PARAMETERS

```
Similarity matrix    Unitary
Mismatch penalty     1
Gap penalty          5.00     K-tuple              4
Gap size penalty     0.33     Joining penalty     30
Cutoff score         1        Window size        500
Randomization group  0
```

SEARCH STATISTICS

```
Scores:      Mean    Median    Standard Deviation
             106     100       6.35
```

```
Times:       CPU                Total Elapsed
             00:00:00.00        00:00:00.00
```

```
Number of residues:           4027
Number of sequences searched:    3
Number of scores above cutoff:   3
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

2. US-09-910-186A-19 (1-1242)
US-08-123-975A-1 Sequence 1, Application US/08123975A

```
Initial Score    =    110    Optimized Score    =    448    Significance    =    0.63
Residue Identity =    43%    Matches            =    546    Mismatches      =    580
Gaps             =    133    Conservative Substitutions    =    0
```

3. US-09-910-186A-19 (1-1242)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

   Initial Score = 99 Optimized Score = 477 Significance = -1.10
   Residue Identity = 44% Matches = 582 Mismatches = 626
   Gaps = 113 Conservative Substitutions = 0

TGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTCTAGAGTCGAGGCC
1290   1300   1310   1320   1330   1340

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-19-inv.res made by bobryen on Thu 7 Nov 102 14:46:49-PST.

Query sequence being compared:US-09-910-186A-19' (1-1242)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-19' (1-1242) with
       File : US08123975A.seq

complement

| | | | | | | | | | | | |
100-|
   -|
N -|
U 50-|
M -|
B -|
E -|
R -|
   -|
O -|
F 10-|
   -|
S -|
E 5-| *
Q -|
U -|
E -|
N -|
C -| *
E -|
S 0-|--|---|---|---|---|---|---|---|---|---|---|
SCORE 0   8 17 25 34 42 51 59 68 76
STDEV   -2   -1   1

PARAMETERS

Similarity matrix	Unitary
Mismatch penalty	1
Gap penalty	5.00
Gap size penalty	0.33
Cutoff score	1
Randomization group	0

K-tuple	4
Joining penalty	30
Window size	500

SEARCH STATISTICS

	Mean	Median	Standard Deviation
Scores:	63	39	21.94

	CPU	Total Elapsed
Times:	00:00:00.00	00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

			Init.	Opt.		
Sequence Name	Description	Length	Score	Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	76	209	0.59	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	76	209	0.59	0
	**** 1 standard deviation below mean ****					
3. US-08-123-975A-6	Sequence 6, Application U	1351	38	442	-1.14	0

1. US-09-910-186A-19' (1-1242)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score	=	76	Optimized Score	=	209	Significance =	0.59
Residue Identity	=	398	Matches	=	246	Mismatches	=	332
Gaps	=	48	Conservative Substitutions	=	48	Conservative Substitutions	0

```
      640       650       660       670       680       690       700       710
TGTACAGCATGTTACCGATGTTCAGAGCCGGCCGATGTACGGATGACGGATGATGAGTAGTGTCAGCGGATTTTGT
                 |||| ||| |||| |||| ||||| |  || |||||| |||||
            CTCGAGCCATGCGTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                    X        10        20        30        40        50

      720       730       740       750       760       770
CAGTGGTGGAAACTTCAGAAGTTTCGTCGGTGAAGTCGTAAACCAGCTGTTCAACCCACCCAGGA------
|| ||  || ||||  ||  |  |||| |||||||  || | |||||| ||| |||| || |||
CATCAAT--ACCTCCATCCTGAACCTGCGGTACGAATCCACCACTCGACCTGTCTCGGCTACGCTTC
         60        70        80        90       100       110       120

      780       790       800       810       820       830       840
ACATAGCAGCTTCAGTAGCTTTGTAACTTTCTTAACGTAGTC--GGAAGAGAAGAAGTGTAAACGGCGAGA
|| |  |||||||| ||| |  || ||| |||  |  ||||    |||||||| |  ||| ||||| ||||
CAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCAGAATCAGATCCACAAGAATCAGATCCAGCGTTCAATCTGGA
         130       140       150       160       170       180       190

      850       860       870       880       890       900
CGGGTTCAGCAGAG---CTTCGTTAACGGAGTTA---------GTCAGAGCGGATACGAGAGATTTACCGT
||||| |||| |||     ||  || | ||||              || ||| |||| || |||  || ||
ATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTC
         200       210       220       230       240       250       260

      910       920       930       940       950       960
GTTCGAATTCCTGAGCACGCAGGTAGTGGAACATGGTGATTGTCCAGTTCGTATTTCTT----GCCGTT
|| ||   ||| || ||| |||  |  ||| || ||||||  |  ||  ||  ||| |
CTTCTGGATCCGTATCCCG-AAATACTTCAACTCCATCTCTCTGAACAATGAATACCACCATCACTGCA
         270       280       290       300       310       320       330

      970       980       990      1000      1010      1020      1030
CGGGAAGCCGTTCGATGTTCGGCCATCAGTTCCAGCGTGAC--CGATGATGTCGGAAGAACAGGTTTTCGATGGAG
||| || || ||  ||  ||  ||   ||  |  |  ||    ||| |||| |   ||| ||  || ||  |||
TGGAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGAAATCATCTGACTCTGCAGGACACTCAGG
         340       350       360       370       380       390       400

     1040      1050      1060      1070      1080      1090      1100
ATGTTTTCCGGTTCGGTTG--------TCGAAGTTGAAAGTCAGGTAGTACTGCTGGATCAGGTCCAGAG
| | | | |  |||||        ||   |||  |||  |||||  |  |||||| |||| ||| ||
AAATCAAACAGCGTGTTGTATTCAAATACTCCAGATGATCAACATCTCGACTACATCA--ATCGCTGGAT
         410       420       430       440       450       460       470

     1110      1120      1130      1140      1150      1160      1170
AGATGTTTTCTCAGCAGCTTCGATGTTAGTTAGTGTCGGAGGTGATTTCTTCGCCTTGTTCAGGTCGTTAGTGA
||| | || |||| |||| |   || || | |||  |||  |  |  || ||  |||| |  |||
CTTCGTTACCATCACCAACAATCGTCTGAATAAGTCCAAAATCTACATCAACGCGCCGTCTGATCGACCAGAA
         480       490       500       510       520       530       540

     1180      1190      1200      1210      1220      1230      1240 X
AGTTGTCTTCAGACGGGGAGAAGAACAGGTCCCAGTTGTTAACTTTGATGCACAGGTCGTTCAGAGCCAT
||| |   | || |||   |  || || || |||  ||  | ||   |  | ||  || |  ||||| ||
ACCGATCTCCAATCTGGGTAACATCCACCGTTCTAATAACATCATGTTCAAACTGGACGAGGTTGTCGTGACAC
         550       560       570       580       590       600       610       620

TCACCGCTACATCTGGAT
|||||| | | || ||
         630       640
```

2. US-09-910-186A-19' (1-1242)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	76	Optimized Score	=	209	Significance	=	0.59
Residue Identity	=	39%	Matches	=	246	Mismatches	=	332
Gaps	=	48	Conservative Substitutions	=				0

3. US-09-910-186A-19' (1-1242)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score	=	38	Optimized Score	=	442	Significance	=	-1.14
Residue Identity	=	40%	Matches	=	524	Mismatches	=	681
Gaps	=	79	Conservative Substitutions	=				0

```
        -GAGAAGAAGGTGTAAACGCGAGACGGGCTTCAGCAGAGCTTCGTTAACGGAGTTAGTCAGCGGATACGAGA
         ||  |  |  || |||  || || ||||  ||||  |  ||  |||   ||||   |    ||  |  ||
        CTCTAAATACATCAACTACCCGACCTGTACATCGGTGAAAAGTTCA-----TCATCCGTCCGAAAATCTAAC
840              850        860        870        880        890        900

        900       910       920       930       940       950       960
        TTTACCGTGTTCGAATTCCTGAGCACGCAGGTAGTGGAACATGGGTATTTGTCCAGTTCGTATTTCTTGCC
        |  |  |  ||||  ||  |  || || |||||  |  ||  ||    |  |  |||||  || |  ||||
        TCTCAGTCGTCCATC--AATGATGACATCGTACGTA----AAGAAGACTACATCTACCTGACTTCTTCAACCTG
        910       920       930       940              950       960       970

        970       980       990       1000      1010                1020
        GTTCGGGGAAGCGTTCGATGTTCGGCATCAGTTCCAGCTGACCGATGA--------TGTCGGAAGACAGGTT
        ||  ||| ||  ||||||| || |  |  || |  |  || | ||   ||   | |   ||  |||  |
        AATCAGGAAATGGCGTGTATACACCTACAAGTACTTCAAGAAGAAGAAGCTTTTCCTGCCTCCGATC
        980       990       1000      1010      1020            1030      1040

        1030      1040      1050      1060      1070      1080      1090      1100
        TTCGATGGAGATGTTTTCCGGGTTCGTTGTCGAAGTGAAAGTCAGGTAGTACTGCTGGATCAGGTCCAGAGA
        |  |  |  ||  |  ||  || | |  |  || ||  | ||  ||  || |  ||  ||  |  ||||  |
        TCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGC-CGACCTACTCTTGCCA
        1050      1060      1070      1080      1090      1100      1110

        1110      1120      1130      1140      1150      1160
        GATG--TTTTCTTCAGCAGCTTCGATGTTAGTGTCGGAGGTGATTCTTCGCCTTGTTGTTCAGGT---CGTTAG
        |  |  |  |  ||  |  ||  ||  ||  |  || | |  |  |  ||  || |  |  |  ||||
        GCTGCTGCTTCAAGAAAGATGAAGAATCTACTGACGAAAATCGGTCTGATCGGTATCCACCGTTTCTACGGAATC
        1120      1130      1140      1150      1160      1170      1180

        1170      1180      1190      1200      1210      1220      1230      1240
        TGAAGTTGTCTTCAGACGGGGAGGAAGAAACAGGTCCCAGTTGTTAACTTTGATGCACAGGTCGTTCAGAGCCA
        |  || |  ||  |  || |  |  |  ||  ||  |  ||  || |  ||   |||  |||   || ||  ||
        TGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCCCAAATGGTACCTGAAGGAAGTTAAACGCAA
        1190      1200      1210      1220      1230      1240      1250

        X
        T
        ACCGTACAACCTGAAACTGGG
        1260      1270      1280
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-20.res made by bobryen on Thu 7 Nov 102 14:35:30-PST.

Query sequence being compared:US-09-910-186A-20 (1-413)
Number of sequences searched:                          3
Number of scores above cutoff:                         3

Results of the initial comparison of US-09-910-186A-20 (1-413) with:
      File : US08123975A.pep
```

```
100-
      |
    N |
 50-| U
      M
      B |
    E |
    R |
      |
  10-| O
      F |
      |
    S |
      |
   5-| E
    Q |
    U |
    E |
      |
    N |
    C |
    E |                                                              *
  0-**|------|-----|-----|-----|-----|-----|-----|-----|-----|----*--|
    S  0    29    58    87   116   144   173   202   231   260
  SCORE
  STDEV  0                       1           1
```

```
                PARAMETERS

Similarity matrix      PAM-150      K-tuple              1
Threshold level of sim.   16%      Joining penalty     20
Mismatch penalty          1        Window size        413
Gap penalty            5.00
Gap size penalty       0.05
Cutoff score           0
Randomization group    0

                SEARCH STATISTICS

           Mean    Median    Standard Deviation
Scores:     97       17           140.59

           CPU              Total Elapsed
Times:  00:00:00.00         00:00:00.00

Number of residues:              1704
Number of sequences searched:       3
Number of scores above cutoff:      3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                                       Init.  Opt.
Sequence Name   Description                            Length  Score  Score  Sig.  Frame
----------------------------------------------------------------------------------------
                      **** 1 standard deviation above mean ****
  1. US-08-123-975A-2 Sequence 2, Application U  850    260    297    1.16      0
                      **** 0 standard deviation from mean ****
  2. US-08-123-975A-3 Sequence 3, Application U  415     17    181   -0.57      0
  3. US-08-123-975A-5 Sequence 5, Application U  439     16    179   -0.58      0
```

```
1. US-09-910-186A-20 (1-413)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =   260   Optimized Score          =   297   Significance =   1.16
Residue Identity =   45%   Matches                  =   189   Mismatches   =    198
Gaps             =    5    Conservative Substitutions =    5                 =     19

        X    10        20        30        40        50        60        70
MALNDLCIKVNNWDLFFSPSEDNFTNDLNKGEETTSDTNIEAAENISDLIQQYYLTFNFDNEPENISIEN
        ||||                                             ---LILDTDLISKIELPSE
APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINE----
X    10        20                        50        60

        80        90       100       110       120       130       140
LSSDIIGQLELMPNIERFPNGKKYELDKYTMFHYLRAQEFEHGKSRIALTNSVNEALLNPSRVYTFFSSDYV
        |  :::     || :  | :    |:   |  ||||  ||:||||| |:||||||||  :|||||
NTESLTDFNVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSPDALLFSNKYYSFFSMDYI
70        80        90       100       110       120       130

       150       160       170       180       190       200       210
KKVNKATEAAMFLGWVEQLVYDFTDETSEVSTTDKIADITIIPYIGPALNIGNMLYKDDFVGALIFSGAVI
        |  :::::  ||| | :: |  |   ||| :  || |:  | |||  |||:    :|:  ||
KTANKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASI
140       150       160       170       180       190       200

       220       230       240       250       260       270       280
LLEFIPEIAIPVLGTFALVSYIANKVLTVQTIDNALSKRNEKWDEVYKYIVTNWLAKVNTQIDLIRKKMKEA
        ||| : |||||  | :: : |: |||||  :||| :|||  :|  :|||:|  |:|||: ||||
LLEFIPELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKA
210       220       230       240       250       260       270       280

       290       300       310       320       330       340       350       360
LENQEAATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINKAMININKFLNQCSVSYLMNSMIPYGVKR
        |  : :| | ||  :|:|  |:|| :|: :||| |:| ||::|   |||||||::||
LNYQAQALEEIIKYRNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEK
290       300       310       320       330       340       350

       370       380       390       400       410     X
LEDFDASLKDALLKYIRDNYGTLIGQVDRLKDKVNNTLSTDIFFQLSKYVDNQ
        |  ::::|  :|  | ||  | : ||  |  |||  |||   |:|| :
LLDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPPDLSIYTNDTILIEMFNKYNSEILNNIIL
360       370       380       390       400     X  410              420
N
```

```
2. US-09-910-186A-20 (1-413)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =    17   Optimized Score          =   181   Significance =  -0.57
Residue Identity =    9%   Matches                  =    41   Mismatches   =    342
Gaps             =     5   Conservative Substitutions =    5                 =     25

        X    10        20        30        40        50        60
MALNDLCIKVNNWDLFFSPSEDNFTNDLNKGEETTSDTNIEAAENISDLIQQYYLTFNFDNEPENI
        |||  :       ||   :  :| |  :|  :  |: :   ::  ||   :    |
RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYF
X    10        20        30        40        50        60        70

        70        80        90       100       110       120       130       140
SIENLSSDIIGQLELMPNIERFPNGKKYELDKYTMFHYLRAQEFEHGKSRIALTNSVNEALLNPSRVYTFFS
```

```
                  |   :     |  : |       |        |  : |::   ::|   :
      NSISLNNEYTIINCMENN-----SGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTIT
         80        90        100       110       120       130
                                                                                  Q

      :          |         |        |        |       |  :  :|::            GCNWQFIPKDEGWTE
      SDYVKKVNKATEAAMFLGWVEQLVLVDFTDETSEVSTTDKIADITIIIPYIGPALNIGNMLYKDDFVGALIFS      X  430
        150       160       170       180       190       200       210

               :           |        | |: |  |     |   :  |:        |    |
      NNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELENEKEIKDLYDNQS
      140       150       160       170       180       190       200       210

                 | | :: |     |  |   :    |  |    |              |  :  |  :|
      GAVILLEFIPEIAIPVLGTFALVSYIANKVLTVQTIDNALSKRNEKWDEVYKYIVTNWLAKVNTQIDLIRKK
      220       230       240       250       260       270       280

               |  :|          |   | |  |       |     |: |   |            :|
      NSGILLKDFWGDYLQYDKPYYMLNLFDPNKYYDVNNVGIRGVMYLKGPRGSVMTTNIYLNSSLYRGTKFPIKK
      220       230       240       250       260       270       280

      MKEALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINKAMININKFLNQCSVSYLMNSMIPY
      290       300       310       320       330       340       350

      YASGNKDNIVRNNDRYIINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITNKCK
      290       300       310       320       330       340       350

                                                            |  X
      GVKRLEDFDASLKDALLKYIRDNYGTLIGQVDRLKDKVNNTLSTDIPFQLSKYVDNQ
      360       370       380       390       400       410       X

      MNLQDNNGNDIGFIGPHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL
      360       370       380       390       400       410 X


3. US-09-910-186A-20 (1-413)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =   16    Optimized Score    =    179    Significance    =   -0.58
Residue Identity =  11%    Matches            =    118    Mismatches      =    340
Gaps             =           20    Conservative Substitutions =     47    Mismatches =    18

          10        20        30        40        50        60        70
      MALNDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITSDTNIEAAEENISLDLIQQYYLTFNFDNEPENISIEN
                  :         | :  ::      |         : |:  | | |  | :    |
      FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQN
      X      10        20        30        40        50        60

          80        90        100       110       120       130       140
      LSSDIIGQLELMPNIERFPNGKKYELDKYTMFHYLRAQEFEHGKSRIALTNSVNEAL---LNPSRVYTFFS
              |  |  |    |  | :       |       | | :   |        |   |: ||  ||
      IIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKKNNSGWKISIRGNRIIWTLIDINGKIKSVFFE
      70        80        90        100       110       120       130

          150       160       170       180       190       200       210
      SDYVKKVNKATEAAMFLGWVEQLVYDFTDETSEVSTTDKIADITIIIPYIGPALNIGNMLYKDDFVGALIFS
            :           |        | | :|  |     |   :  |:        | |: |
      YNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFS
      140       150       160       170       180       190       200

          220       230       240       250       260       270
      GAVILLE------FIPEIAIPVLGTFALVSYIANKVLTVQTIDNALSKRNEKWDEVYKYIVTNWLAKVNTQ
                   | | : |  |   |:       |  | |  |  |    | |  |   |
      IFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSK
      210       220       230       240       250       260       270       280

          280       290       300       310       320       330       340
      IDLIRK--------KMKEALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINKAMININKF
                |:         |           | :  |                |
      YINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEF
      290       300       310       320       330       340       350

          350       360       370       380       390       400       410
      LNQCSVSYLMNSMIPYGVKRLEDFDASLKDALLKYIRDNYGTLIGQVDRLKDKVNNTLSTDIPFQLSKYVDN
                |:               |        ::
      YNTIQIKEYDEQPIYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL
      350       360       370       380       390       400       410       420

      X
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-21.res made by bobryen on Thu 7 Nov 102 14:47:13-PST.

Query sequence being compared:US-09-910-186A-21 (1-1242)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-21 (1-1242) with:
    File :US08123975A.seq

```
100-
N   -
U 50-
M   -
B   -
E   -
R   -
    -
O   -
F 10-
    -
S   -
E 5-
Q   -
U   -
E   -
N   -
C   -
E   -                                                    *
S   -
  0 -----|----|----|----|----|----|----|----|----|----|----|----|
SCORE 0  13| 27  40  53  67  80  93 107  120
STDEV    -4  -3  -2  -1   0   1
```

PARAMETERS

Similarity matrix   Unitary
Mismatch penalty   1   K-tuple   4
Gap penalty   5.00   Joining penalty   30
Gap size penalty   0.33   Window size   500
Cutoff score   1
Randomization group   0

SEARCH STATISTICS

Scores: Mean   Median   Standard Deviation
                98   89   18.48

Times: CPU   Total Elapsed
       00:00:00.00   00:00:00.00

Number of residues: 4027
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
                                                                          Init. Opt.
Sequence Name   Description                               Length Score Score Sig. Frame
-------------   -----------                               ------ ----- ----- ---- -----
                **** 1 standard deviation above mean ****
1. US-08-123-975A-6 Sequence 6, Application U 1351  120  320  1.19    0
                **** 0 standard deviation from mean ****
2. US-08-123-975A-4 Sequence 4, Application U 1338   88  394  -0.54   0
3. US-08-123-975A-1 Sequence 1, Application U 1338   88  394  -0.54   0
```

1. US-09-910-186A-21 (1-1242)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score   = 120   Optimized Score   = 320   Significance = 1.19
Residue Identity = 40%   Matches   = 359   Mismatches   = 486
Gaps   =   Conservative Substitutions = 46

```
                      x         10        20        30        40
                      ATGGCTCCAGGAATCTG------TATCGACGTCGACAACGAGGAGGACTTGTT
                                           || ||||||||||  ||||
         CAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGCTAAATCTACATCAACGGTAAACTGGA
         450       460       470       480       490       500       510

           50        60        70        80        90       100       110
         CTTCATCGCTGACAAGAACTCCTTCTCCGACGACTTGTCCAAGAAGACGAGAA---TCGAGTACAACACCCA
                  ||| || | |   | |||   | ||  ||||| |||  |||    ||| ||  || || |
         ATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGACGGGTGA
         520       530       540       550       560       570       580       590

          120       130       140       150       160       170       180
         GTCCAACTACATCGAGACGACTCCCAATCAACGAGGTGATCTTGACACCGACTTG---ATCTCCAAGAT
              |||| |  ||      | ||  |||   |||  |  ||| || |||    | |||||  ||||
         CATCGATCGTACCCAGTCATCGTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATAT
         600       610       620       630       640       650       660

          190       200       210       220       230       240
         CGAGTTGCCATCCGAGA------ACACCGAGTCCTGACTGACTCAACGTCGACGTCCCAGTCTCACGA
         |||  ||| | |  |       | || |||||  | || || | ||||  ||  || |  |||| |||
         CGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTGTACAA
         670       680       690       700       710       720       730

          250       260       270       280       290       300       310
         GAAGCAACCAGCTATCAAGAAGATTTCACCGGACGAGAACACCATCTTCCAATAACCGTACTCTCAGACCTT
              |||||| ||| |  |||||   |||  |||| | |   |  ||||| ||||||  |  |||||||
         CAAAGAATACTATATGTTCAATGCTGGTAACAAGAACCTCTTACATCAAACTGAAGAAGAACTCTCCGGTTGG
         740       750       760       770       780       790       800

          320       330       340       350       360       370       380
         CCCTTTGGACATCAGAGACA---TCTCCTTGACCTCTTCCTTCCGTGTTCTCCAACAAGGT
              |||| ||| ||||       |||| || |||  | |||| |  || || |||| ||||
         TGAAATCCTGACTCGTTCCAAATACAACCAGAACTTCTAAAATACATCAACTACCGCGACCTGTACATCGGGTGA
         810       820       830       840       850       860       870

          390       400       410       420       430       440       450
         CTACTCCTTCTTCTCCATGGACTACATCAAGAGCTGCTAACAGGTCGTCGAGGCGGTTGTTCCGCTGGTTG
            |  ||| ||| |||  || |||||   ||  ||||| |  ||| | ||||||| |  |||||| |||
         AAAGTTCATCATCCGTCCGCAAATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAGAAGAGCTACAT
         880       890       900       910       920       930       940       950

          460       470       480       490       500       510       520
         GGTCAAGCAGATCGTCAAC--GATTTCGTCATCGAGGCTA-ACAAGTCCAACACCATGGACAAGATTGCCGA
          ||| ||| ||||| |     |||| ||| ||| |||    | |||| | || |||| || |||| | ||
         CTACCTGGACTTCTTCAACCTGATCAGGAATGGCGTGATACACCTACAGTACTTCAAGAAGAAGAGA
         960       970       980       990      1000      1010      1020

          530       540       550       560       570       580       590
         CATCTCCTTGATTGTCCATACATCGGTTGCCTTGAACGTCGGTAACAAGGTAAGGGTAACTTCGA
         | | ||| || | |||    |||| ||  ||||| | ||| ||||| ||||| ||||  |||||
         AAAGCTTTCCTGGCTCCGATCTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAGAGAATACGACGA
         1030      1040      1050      1060      1070      1080      1090

          600       610       620       630       640       650       660
         GAA------CGCTTTCGAGATCGCTGGTGCCTCCATCTTGTTGGAGTTCATCCCAGAGTTG--TTGATCCC
         1040      1050      1060
```

2. US-09-910-186A-21 (1-1242)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score   =   88   Optimized Score   =   394   Significance = -0.54
Residue Identity   = 41%   Matches   =   459   Mismatches   =   582
Gaps   =   Conservative Substitutions   =   77   0

3. US-09-910-186A-21 (1-1242)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score   =   88   Optimized Score   =   394   Significance = -0.54
Residue Identity   = 41%   Matches   =   459   Mismatches   =   582
Gaps   =   Conservative Substitutions   =   77   0

CTCAGG
1090

```
           880        890        900        910        920        930        940

           1120       1130       1140       1150       1160       1170       1180
GAGAACAAGTTGTAC-TTGATCGGTTCCCGCTGAGTACAGAGAAGTCCAAGGTCAACAGTACTTGAGACCAT
|-|||-|||||-|-||-|||||||||||||-|||-|||||||-|||||||||-||-|||||||-||||||||
AATATCGTTCGCAACAATGATCGTGTATACACGTGTAGT-TAAGAACAAAGAATACCGTCTGGCTAC
          950        960        970        980        990       1000       1010

          1190       1200       1210       1220       1230       1240 X
CATGCCATTCGACTTGTCCATCTACACCAACGACACCATCTTGATCGAGATGTTCTAA
||  |||  ||| | |||||||  || |||||  |||||||||||
CA----ATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGGTTGGTAATCTGT
1020       1030       1040       1050       1060       1070 X       1080

CTCAGG
1090
```

```
AACATCATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGACCTGTCTCGCTACGGCT
50         60         70         80         90        100        110

280        290        300        310        320        330        340
GAGAACACCATCTTCCAAT-ACCTGTACTCTCAGACCTTCCCCTTTGGACACTCAGAGACATCCCT-----TG
TCCAAAATCACATCGGTTCTAAAGTTAACTCGATCGACCAAGAATCAGATCCAGTTGTTCAATCTG
120        130        140        150        160        170        180        190

350        360        370        380        390        400        410
ACCTTCCTGCGACGACGCCCTGCGTGTTCTCCAACAAGGTCTACTCCTTCTCTCCATGGACTACATCAAG
GAATCTTCCAAAATCGAAGTTATCCTG-----AAGAATGCTATCGTATACAACTCTATGTAC-------
200        210        220        230        240

420        430        440        450        460        470        480
ACTGCTAACAAGGTCGTCGAGGCCGGTTGTTCGGTCGATCGTATCCCGAAATACTTCCAACTCCATCTCTGAACAAT
-----GAAAACTTCTCCACCTCCTTCGGATCCGTATCCGAAATCACTGTCAAGCAGATCGTCAAGCAGATTCGTCATC
250        260        270        280        290        300        310

490        500        510        520        530        540        550
GAGGCTAACAAGTCCAACACCATGGACAAGAGATTGCCG-------ACATCTCCTTGATTGTCCCATACATCGGT
GAATACACCACCATCAACTGCATGGAAAACAATTCTGTTGCAAAGTATCTCTGAACTACGGTGAAATCATC
320        330        340        350        360        370        380

560        570        580        590        600        610        620
TTGGGCCTTGAACGTCGGTAACGAGACCGCCAAGGGTAACTTCGAGAACGCGTTTCGAGATCGCTGGTGCCTCC
TGGACTCTGCAGGACACTCCAGGAAATCAAACACGTGTTGTTATTCAAATACTCTCAGAT-------GATCAAC
390        400        410        420        430        440        450

630        640        650        660        670        680        690
ATCTTGTTGGAGTTCATCCCAGAGTGTTGATCCCAGTCGTCGGTGCCTTCTTGTTGTGGAGTCCTACATCGAC
ATCTCTGACTACGTACGGCTGGATCTTCGTTACCATCAACAATACCGTCGAATAACTCCAAAAATCTAC
460        470        480        490        500        510        520

700        710        720        730        740        750
AACAAGAAC---AAGATCATCAAGACCATCGACAAGCCTTTGACCAAGAGAAACG-------AGAAGTGG
ATCAACGGCGTCTGATCGACCAGAAACCGATCTCAAATCTGGGTAACATCCACGCTTCTAATAACATCATG
530        540        550        560        570        580        590

760        770        780        790        800        810        820        830
TCCGACATGTACGGTTTGATCGTCGGCGCCAATGGTTGTCCCACCGTC-AACACCCAATTCTACACCATCAAGGA
TTCAAACTGGACGGTTGTCGTGACACTCACCGCTACACTGGATCAAATACTTCAATCTGTTCGACACAAAGAA
600        610        620        630        640        650        660

840        850        860        870        880        890
GGGTATGTACAAGGCCTTGAA------CTACCAGGCCCAAGCTTTGGAGGAGATCATCAAGTACAGAGATACAAAC
CTGAACGAAACAAAGAAATCAACGACACCGATCTACGACAACAGTCCAATTCTGTATCCTGAAAGGACTTCTGGGGT
670        680        690        700        710        720        730        740

900        910        920        930        940        950        960
ATCTACTCCGAGAGGAGAAGTCAACAAGTCGAACATTAACATGGACTTCAACGACAATCCCAAGCTGAACGAGGGT
GACTACCTGCAGTACGACGACAAACCGTACTACATGCTGAATCTGACG-------
750        760        770        780        790        800

970        980        990       1000       1010       1020       1030       1040
ATTAACCAGGCCATCGACACAACAACTTCATCACAGGTGTTCCGTCCTACTTGATGAAGGAGAGATG
-TCAACAATGTAGGTATCCGCCGTTACACGTACCTGAAAGGTCCGCGCCTGTTCTGTTTGTTATGACTACCAACAT-
810        820        830        840        850        860        870

1050       1060       1070       1080       1090       1100       1110
ATTCCATTGGCGCGTCGAGAAGTTGTTGGACTTCGACAACACCCTGAAGAAGAAACTTGTTGAACTACATCGAC
CTACCTGAACTCTTCCTCCCCTGCCGTACCGTGGTAC--CAAATTCATCATCAAGAAATACCGGTCTGGTAACAAGGAC
880        890        900        910        920        930        940
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-21-inv.res made by bobryen on Thu 7 Nov 102 14:47:31-PST.

Query sequence being compared:us-09-910-186A-21' (1-1242)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

Results of the initial comparison of US-09-910-186A-21' (1-1242) with:
    File : US08123975A.seq                              Complement
```



```
              7   14    22    29    36    43    51    58    65
100-
    -
    -
 50-
    -
    -                                                              *
 10-
    -
  5-
    -                                                         *
  0-
     -7    -9    -7    -5    -3    -2     0
SCORE 0
STDEV

                    PARAMETERS
Similarity matrix   Unitary
Mismatch penalty          1
Gap penalty            5.00    K-tuple                 4
Gap size penalty       0.33    Joining penalty        30
Cutoff score              1    Window size           500
Randomization group       0

              SEARCH STATISTICS
Scores:       Mean      Median    Standard Deviation
               63         62            2.31

Times:        CPU                 Total Elapsed
          00:00:00.00            00:00:00.00

Number of residues:        4027
Number of sequences searched:  3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                         Init. Opt.
Sequence Name   Description                    Length Score Score Sig. Frame
-------------   -----------                    ------ ----- ----- ---- -----
1. US-08-123-975A-4  Sequence 4, Application U   1338   65   457  0.87   0
2. US-08-123-975A-1  Sequence 1, Application U   1338   65   457  0.87   0
3. US-08-123-975A-6  Sequence 6, Application U   1351   61   448 -0.87   0

1. US-09-910-186A-21' (1-1242)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =   65   Optimized Score       =   457  Significance =  0.87
Residue Identity =  42%   Matches               =   556  Mismatches   =   657
Gaps             =  108   Conservative Substitutions =  0

          x        10        20        30        40
        TTAGAACATCTCGATCAAGATGGTGTCGTTGGTGTAGATG--GACAAGTCG
        ||||||||  ||||| ||  |  ||||||||  ||||||     ||| |||||
CTGCTGTCTACCTTCACTGAATACATCAAGAACATCAATAACCTCCCATCCTGAACCTGCGCTACGAATCC
  20        30        40        50        60        70        80

 50        60        70        80        90       100       110
AATGGCATGATGG--TCTTCAAGTACTGTTGTGACCTTGGACTTCTTCGTACTCAG-----CGGAACCGATC
||| |||||||     | ||||  || |||  ||   |||   || |||||||||           ||||||||
AATCACCCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATC
  90       100       110       120       130       140       150       160

 120       130       140       150       160
AAGTACAACTGTTCTCGTCGATGTAGTTCAA----------CAAGTTCTTCTTCAGGGTGTGTCG--
||||||| |||| ||  || ||| ||| |||            |  | ||||||  |  || |  ||||
GACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTA
 170       180       190       200       210       220       230

          170       180       190       200       210
-------AAGTCCAACAACTTCTGACGGCCAATGGAAT--------CACTTCTTCATCAAG
          || |  | | || ||| | | |    |||           |||||||  ||| ||||
TACAACTCTATGTACGAAAACTTCTCCACCTCTTGGATCCGATCCCGAAATACTTCAACTCCATCTCT
 240       250       260       270       280       290       300

 220       230       240       250       260       270       280
TAGGAGACGGACAACCGTTGATGAAGTTGTTGATGTTGCGATGGCCTGGTTAATACCCTCGTTCAGCTTG
|||  ||| ||||  || ||||||| |||| ||  ||||  |||  |   |  |   |||  ||  ||||||
CTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTCGGAAAGTATCTCTGAACTACGGT
 310       320       330       340       350       360       370

 290       300       310       320       330       340       350
GAGTTGATGTCGTTGAAGTCGATGTTAATGTTGGCACTTCTTCCTTCTCCGGAGTA--GATGTTGTATCGTACT
|| ||| |  ||| |  | | ||| || |||| ||  | ||||  | ||  |||        ||  |  ||||||
GAAATCATCTCG--ACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGA
 380       390       400       410       420       430       440

 360       370       380       390       400       410       420       430
TGATGATCTCCTCCAAAGCTTGGGCCTGGTAGTTCAAGGCCTTGTAC-ATACCCCTTGATGGTGTAGAAT
| | |||||| || | |||| | || | ||  ||| |   ||||| |    ||  |  ||  | ||| |||
TCAACATCTCGACTACTACATCAGTCGGATCTTCGTTACCACCAACAATCGTCTGAATAACTCCAAAA
 450       460       470       480       490       500       510

          440       450       460       470       480       490
TGGGTGTGACGG-----TGGACAACCATTGGGCGACGATCAAACCGATCTCCAATCTGGGTAACATCCACGCTTCGTTC
||| ||  ||||        ||||| ||| ||| ||  || |   |||||  ||  ||||  ||||| ||  || |||||
TCTACATCAACGGCCCGTCGATCGACGAAAATCCAATCTCCAATCTGGGTAACATCGAGGACCACTTCGTTTCTCGTTTC
 520       530       540       550       560       570       580       590

 500       510       520       530       540       550       560
TCTTGGTCAAAGCGTTGCGATGGTCGTTGCTGACCTTGATGATCTTGTTCTTGTTGTGGTGCGATGGGAGAAG
| ||| || | | |  |    ||| |||| |  | |||  |  ||||||  |||  ||||  |  || |||||||
TCATGTTCAAA--CTGGACGGTGTCGTGACACTC-ACCGTACATCTGGATCAATACTTCAATCGTGTTCG
 600       610       620       630       640       650       660

 570       580       590       600       610       620       630
GCACCGACGACTGGGATCAACAACTCTGGGA--TGAACTCCAACAAGATGAGGCACCAGCGATCTCGAAAG
|| || || |   |||  || || | |||        || || || |||| || |  |  || |||| |||
ACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACGACCAGTCCAA---TTCTCGTATCCTGAAAG
```

(The main body of this page consists of a dense, sideways-oriented nucleotide sequence alignment with position numbering.)

2. US-09-910-186A-21' (1-1242)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score = 65   Optimized Score = 457   Significance = 0.87
Residue Identity = 42%   Matches = 556   Mismatches = 657
Gaps = 108   Conservative Substitutions

```
                    950       960       970       980       990      1000
             AAAGGGAAGGTCTGGAGTAGTACAGGTATTGGA-AGATGGTGTTCTCGTCGGTGAAAATCTTCTTGATAGCTGG
              ||       ||| || |  ||        |  ||||| |||| ||| |  |  |||| | ||| |||
920          TCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAATCTTGTCTCGTCTGGAAATC------CCGGACG
             920       930       940       950       960       970

                   1000      1010      1020      1030      1040      1050
             TTGCTTCTCGTAGACTGGGACGTCGAGCGGTGAGAGTCAAGGACTCGGTGTTC----TCGGATGGCAACT
              ||| |||    |    |||   |    | ||  |  |  || |  |||      |  |||||| |
1010         TTGGTAATCTGTCTGCAGTAGTTGTA-ATGAAATCCAAGAACGACCAGGGTATCAACTAACAAATGCAAAT
             1010      1020      1030      1040      1050      1060      1070

                   1060      1070      1080      1090      1100      1110      1120
             CGATTCTGGAGATCAAGTCGGTGTCCAAGATCAACTCGTTGATTGGGAAGTCGTTCTCGATGTAGTTGGACT
             1080      1090      1100      1110      1120      1130      1140

                   1130      1140      1150      1160      1170      1180      1190      1200
             GAATCTGAGGACGAACAACAATGGTAACGATCGGTTCATCGGTTCCACCAGTTCAACAATATCGCTAAACT
             1150      1160      1170      1180      1190      1200      1210

                   1210      1220      1230      1240 X
             AAGTCCTCGTTGTCGAC---GTCGATACAGATTCCTGGAGCCAT
             1210

             GGGTG-TTGTACTCGGATCGTCCGATCCTTGGACAAGTCGTCGGAGGAGGAGGTTCTTGTCAGCGATGAAGAAC
                                 TCATCCCGGTTGATGAGACGTTGGGGTGAACGTCCGGCTTGTAACCCGGGAAAGCTT
                                 1290      1300      1310      1320      1330
```

3. US-09-910-186A-21' (1-1242)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

```
Initial Score      =  61    Optimized Score     =  448    Significance = -0.87
Residue Identity   =  39%   Matches             =  519    Mismatches   =  713
Gaps               =  68    Conservative Substitutions = 0
```

```
                    X         10        20        30        40        50
                    TTAGAACATCTCGATCAACAATGGTCGTCGTTGGTGTGTAGATGGACAAGTCGAAT
                     |||       |  ||||   |||| ||| |  |||  | || |  |
             ATGGCTTTCAACAAATACAAATTCCGAAATCCTGAAACAATATCATCCTGAAACCTGCCGTTACAAAGACAACAAT
             10        20        30        40        50        60        70

                    60        70        80        90       100       110       120
             GGCATGACGATGGTGTCTTCAAGTACTTGTTGACCTTGGACTTCTCCTACTACCGGAACCGGATCAAGTACAACTTG
             GCTAGATCGATCTGTCTGGTTTACGGTGCTAAAGTTGAAGTTGAAGTGTGTGTAACTGAATTGACAAGAACCAG
             80        90       100       110       120       130       140

                   130       140       150       160       170       180       190
             TTCTGCTGCGATGATGCGAGTTCAACAAGTTCAACAACTCGTAGCTGTTGGCTAGTCCGTATCCTGGATAGTTGTTGTTCAACTTCTCGACGGCC---
             TTCAAACTGACCTGTGGTTGTACCCGGTTGATGAGTTGTTGGGTGGTTCGTATCCTGGATCTGTTCTGTGTTTCCAACTTCTCGACGGCC---
             150       160       170       180       190       200       210

                   200       210       220       230       240       250       260
             --AATGGAATCATCTTCTTCATCAAG--TAGGAGACGGAACAACCGTTGACGTTGATGAAGTTGTTGATGTTGTCGAT
             TCCTTGGACTTCGTCTGGTTCCTTACGGTGCTAAAGTTCTCGTTCTTCTGTTTCAAGAAAGCTTGAAGCTTCCAGAAATACATC
             220       230       240       250       260       270       280

                   270       280       290       300       310       320       330
             GGCCTTGGTTAATACCCTCGT--TCAGCTTGGAGTTGATGTCGTTGAAGTCGCATGTTAAATGTTGGACTTCTCC
             CACAATGAATACAACCACCATCACAACCAACTCGTTGTTGGAGATGCTCCCATCCCGGGTAACCGT
             290       300       310       320       330       340       350       360

                   340       350       360       370       380       390       400
             TTTCCGGAGTAGATGTTGTATCTGTACTTGACTGATCTCCTCCAAAGCTTGGGCCTTGGTAGTTCAAGGCCTTG
             290       300       310       320       330       340       350       360       370       380       390       400
```

```
                    370       380       390       400       410       420
             ATCATCTGGACTCTGATCGATCGATATCAACGGTAAGA------CCAAATCTGTATTCTTCGAATACACACCGT
              |||  |||| || | |  |  |  | | || |  | |        |   ||| | |  ||  ||| |  |||
410          TACATACCCTCCTTGATGGTGTGTAGAATTGGGTGTGACGGTGGACAACCCAT---TGGGCGACGATCAAACC
             410       420       430       440       450       460       470

                   430       440       450       460       470       480       490
             GAAGACATCTGAATACATCATCGCTGGTTCTTCGTTCTTACCATCACCAATAACCTGAACAATGCTAAAATC
             430       440       450       460       470       480       490

                   480       490       500       510       520       530
             GTACATGTCGGACCACT--TCTCGTTCTTCTTGTCAAG-CGTTGTCGATCGTCTTGATGATCTTG---TTC
             GTTGTTGTCGGTGAGGTCGTTCATGCTCTTGGGTGTC
             500       510       520       530

                   540       550       560       570       580       590       600
             TACATCAACCGGTAAACTGGAATCGTTCATCGGTTACTCGAGCCGTGAAGTTATCGCTAACGGTGCAAATC
             TTGTTGTCGATGTAGGCTCCAGCGGTTCGATCAACAAGAGGCACCGACGTGGATCAACAACTCTGGGATGAACTCCAAC
             500       510       520       530       540       550       560       570

                   610       620       630       640       650       660       670       680
             ATCTTCAAACTGACGGTGACACTGGCTCGGTGACCTACCCCAGTTCATCGTGGATGAAATACTTCTCCATCTCCAACAAC
             AAGATGGAGGCACCAGCGATCTCCAAAGCGTTCGAAGTTACCCTTGGCGGTGTCGTTCTTACTGCGACGTTCAAG
             650       660       670       680       690       700       710

                   690       700       710       720       730       740       750
             GCCAAACCGATG-TATGGGACAATCAAGGAGATGTCGGCAATCTTGTCCATGGTGTTGGACTTGTTGGTTAGCCTC
              |||   ||||   |  ||||  | |   || |  |||    |||| |    |||||||  |  ||| |||| |||
             GAACTCTGGTTCCAGTGCCAATGCCAGTTCAACTGTGTAA---CAAGAACTTCTTACATCAA
             690       700       710       720       730       740       750

                   760       770       780       790       800       810
             GATGACGAAATCGTTGACGATCTG-----CTTGACCCAACAGCGAACAATACAACCAGAACTCTAAATACATCAA
             GGTAATCCCGCTGATGTACAACAAGAATACTACTATGTTCAATGTCGTGTAA---CAAGAACTCTTACACTGGTTGTT
             760       770       780       790       800       810

820          ACTGAAGAAGACTTCCGGTTGTGTGAAATCCTGACTGTTCCAAATACCAGACTGTGACGACCTGT
                                              AGGAGTAGACCT-TGTTGGAGACAGC----AGGG
             790       800       810       820       830       840       850

                   820       830       840       850       860       870
             AGCAGTCTTGATGTAGTCCATGGAGAAG-------AAGGAGTAGACCT-TGTTGGAGACAGC----AGGG
             CTACCCGGACCTGTACATCGGTGAAAGTTCATCATCCGCAAATCTAACTCCATCAATGATGA
             860       870       880       890       900       910       920

                   880       890       900       910       920       930
             CGTCGT----CGAAGGAGAGGTCAAGGA----GATGTCT-----CTGATGTCCAAAGGGAAGGTCTGAGAGTA
             CATCGTACGTAAAGAAGACTACATCTCACCTGGCTTCTTCAACCTGAATCAGGAGATGGCGTGTATACACCTA
             930       940       950       960       970       980       990

                   940       950       960       970       980       990      1000      1010
             CAGGTATTGGAAGATCGTGTTCTCGGTGTGTCTCCGGTGAAAATCTTCTTGATAGCTGGTTGCTCCTCGTAGACTCTGGGAC
             CAAGTACTTCAAGAAGATGAAGATACGACGAACAGCCGACTACTCTTGCCAGTGTCGTGTTCAACTGGTATACACCTA
             1000      1010      1020      1030      1040      1050      1060      1070

                  1020      1030      1040      1050      1060      1070      1080
             GTCGACGGTGAAGTCAGTCAAGGAGTCTTCAAGGATCGTTGTCTTGTCGCGATGAGATCAAGAAGTCGGGTGTC
             CATCCAGATCAAAGAATACGACGAACAGCCGACTACTCTTGCCAGTGTCGTGTTCAACTGAAAAGATGAAGAATC
             1080      1090      1100      1110      1120      1130      1140

                  1090      1100      1110      1120      1130      1140
             CA-AGATCAACTCG--TTGATTGGGA-AGTCGTTCTCGATCGGTATCGGTATCGATCGGTGTTG----TACTCGAT
             TACTGACGAAATCGGTCGATCGTTACGAGTAATCGAAGAATACAAAGA
             1150      1160      1170      1180      1190      1200      1210

                  1150      1160      1170      1180      1190      1200      1210
             TCTTCGTTGGACAAGTCGTCGGAGGAGGAGGTTCTTGTCAGCGATGAAGAACAAGTCGTCGTTGTCGAC
             CTACTTCTGCATCCTCCAAATGGTACGTGAGGAAGGAGTAAACGCAACCGTACAACCTACAACCGT
             1150      1160      1170      1180      1190      1200      1210
```

us-09-910-186a-21-inv.res

```
     1220      1230      1240      1250      1260      1270      1280

1220      1230      1240 X
GTCGATACAGATTCCTGGAGCCAT
  | |   ||  ||  |
TTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAAC
1290      1300      1310      1320      1330
```

```
> O <
O| |O   IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-22.res made by bobryen on Thu 7 Nov 102 14:35:52-PST.

Query sequence being compared:US-09-910-186A-22 (1-413)
Number of sequences searched: 3
Number of scores above cutoff: 3

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-2	Sequence 2, Application U	850	412	412	1.16	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-3	Sequence 3, Application U	415	22	185	-0.57	0
3. US-08-123-975A-5	Sequence 5, Application U	439	20	184	-0.58	0

1. US-09-910-186A-22 (1-413)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

```
Initial Score   =   412   Optimized Score      =   412   Significance =  1.16
Residue Identity = 100%   Matches              =   412   Mismatches   =     0
Gaps            =     0   Conservative Substitutions =   0
```

```
              x        10        20        30        40        50        60        70
MAPGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENTESLT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENTESLT
    x        10        20        30        40        50        60        70

         80        90       100       110       120       130       140
DFNVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIKTANKV
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DFNVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIKTANKV
         80        90       100       110       120       130       140

        150       160       170       180       190       200       210
VEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASILLEFIP
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
VEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASILLEFIP
        150       160       170       180       190       200       210

        220       230       240       250       260       270       280
ELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKALNYQAQ
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKALNYQAQ
        220       230       240       250       260       270       280

        290       300       310       320       330       340       350       360
ALEEIIKYRYNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYIMKKMIPLAVEKLLDFDN
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ALEEIIKYRYNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYIMKKMIPLAVEKLLDFDN
        290       300       310       320       330       340       350

        370       380       390       400       410  x
TLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMF
|||||||||||||||||||||||||||||||||||||||||||||||||| x
TLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKD
        370       380       390       400       410  x                   430

N
```

2. US-09-910-186A-22 (1-413)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

```
Initial Score   =    22   Optimized Score      =   185   Significance = -0.57
Residue Identity =   8%   Matches              =   342   Mismatches   =    37
Gaps            =     3   Conservative Substitutions =   31
```

```
              x        10        20        30        40        50        60
MAPGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSEN
|||||:|: |||    : |  ||    :|                       |  :  || ||   |:|
RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYF
    x        10        20        30        40        50        60        70

         70        80        90       100       110       120       130
TESLTDFNVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIK
```

```
                                                                                  *
100 -|- |- |- |- |- |- |- |- |-
     -|
N    -|
U 50 -|
M    -|
B    -|
E    -|
R    -|-

O    -|
F 10 -|-

S    -|
E  5 -|
Q    -|
U    -|
E    -|      *
N    -|
C    -|
E  0 -|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
S   0   46  92 137 183 229 275 320 366 412
SCORE 0  46  92 137 183 229 275 320 366 412
STDEV 0   0   0   0   0   1   1   1   0
```

```
                    PARAMETERS
Similarity matrix    PAM-150         K-tuple             1
Threshold level of sim.  16%
Mismatch penalty     1               Joining penalty    20
Gap penalty          5.00            Window size       413
Gap size penalty     0.05
Cutoff score         1
Randomization group  0

                  SEARCH STATISTICS

Scores:        Mean      Median       Standard Deviation
               151       21           225.75

Times:      CPU                 Total Elapsed
            00:00:00.00         00:00:00.00

Number of residues:               1704
Number of sequences searched:        3
Number of scores above cutoff:       3
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
                                                              YTNDTILIEMF
                                                              |-|  |||||||
                                                              IPKDEGWTE
                                                                      X
```

```
NSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVITNNRLN
        80        90       100       110       120       130       140
```

```
140 TANKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALVGNETAKGNFENAFEIAGASIL
        150       160       170       180       190       200       210
```

```
NSKIYINGRLIIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGIL
    150       160       170       180       190       200       210
```

```
LEFIPELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSIVNTQFYTIKEGMYKAL
    220       230       240       250       260       270       280
```

```
KDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVG---IRGIYMYLKGPRGSVMTTNIYLNSSLIYRGTKFIIKKYA
220       230       240       250       260       270       280
```

```
NYQAQALEEIIKYRYNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEKL
    290       300       310       320       330       340       350
```

```
SGNKDNIVRNNDRVYINVVVKNEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKMN
    290       300       310       320       330       340       350
```

```
LDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMF
    360       370       380       390       400       410 X
```

```
LQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTIGCSWEFIPVDDGWGERPL
350       370       380       390       400       410 X
```

3. US-09-910-186a-22 (1-413)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

```
Initial Score    =  20   Optimized Score            =  184   Significance = -0.58
Residue Identity =  11%  Matches                    =   50   Mismatches   =  327
Gaps             =  32   Conservative Substitutions =   32
```

```
x MAPGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIEND---FPINELILDTDLISKIELPSENT
          10        20        30        40        50        60
```

```
FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFL
x      10        20        30        40        50        60        70
```

```
70 ESLTDFNVDVPYYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIKT
        80        90       100       110       120       130       140
```

```
DFPSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIKWTLIDINGKTKSV--FFREYNIRED
80        90       100       110       120       130       140
```

```
ANKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALVGNETAKGNF----------
    150       160       170       180       190
```

```
ISEYINRWFFVTITPNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTEL
    150       160       170       180       190       200       210
```

```
-----ENAFEIAGASILLEFIPELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWL
    200       210       220       230       240       250       260
```

```
SQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRD
220       230       240       250       260       270       280
```

```
STVNTQFYTIKEGMYKALNYQAQALEEIIKYRYNIYSEKEKSNINIDFNDINSKL------NEGINQAIDN
    270       280       290       300       310       320       330
```

```
LYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQI
    290       300       310       320       330       340       350
```

```
INNFINGCSVSYLMKKMIPLAVEKLLDFDNTLKRNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSI
    340       350       360       370       380       390       400
```

```
KEYDEQPPYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQF
360       370       380       390       400       410       420       430
```

```
    410
```

```
> O V
Ol¡O  IntelliGenetics
> O V

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-23.res made by bobryen on Thu 7 Nov 102 14:47:57-PST.

Query sequence being compared:US-09-910-186A-23 (1-1200)
Number of sequences searched:          3
Number of scores above cutoff:         3

      Results of the initial comparison of US-09-910-186A-23 (1-1200) with:
          File : US08123975A.seq
```

```
100-
    -
    -
 N  -
 U 50-
 M  -
 B  -
 E  -
 R  -
    -
 O  -
 F 10-
    -
 S  -
 E  5-
 Q  -
 U  -
 E  -                                  *
 N  -
 C  -
 E  -                                                          *
 S  0----|---|--|--|--|--|---|---|---|--|---|--|--|--|--|
SCORE 0| 10  20  30  40  51  61  71  81  91
STDEV -6 -5  -4  -3  -2  -1   0   1
```

```
                    PARAMETERS

Similarity matrix    Unitary
Mismatch penalty          1
Gap penalty            5.00      K-tuple                4
Gap size penalty       0.33      Joining penalty       30
Cutoff score              1      Window size          500
Randomization group       0

                SEARCH STATISTICS

                                   Standard Deviation
Scores:        Mean      Median        11.55
                77         72
        CPU                          Total Elapsed
Times:  00:00:00.00                  00:00:00.00

Number of residues:        4027
Number of sequences searched:  3
Number of scores above cutoff:  3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                         Init. Opt.
                                            **** 1 standard deviation above mean ****
Sequence Name    Description            Length Score Score Sig. Frame
------------------------------------------------------------------------

                      **** 1 standard deviation above mean ****
  1. US-08-123-975A-6 Sequence 6, Application U 1351   91  406  1.21   0
                      **** 0 standard deviation from mean ****
  2. US-08-123-975A-4 Sequence 4, Application U 1338   71  304 -0.52   0
  3. US-08-123-975A-1 Sequence 1, Application U 1338   71  304 -0.52   0

  1. US-09-910-186A-23 (1-1200)
     US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    91   Optimized Score       =    406   Significance  =   1.21
Residue Identity  =   428   Matches  =  492   Mismatches  =  571
Gaps              =   100   Conservative Substitutions  =    0
```

```
              X        10        20        30        40        50
         ATGTCCCTGTACAACAAGACCCTTGACTGATGAGAGCTGCTGGTGAAGAACA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
     CTGTTTCCTTCTGGATCCGTATCCCGAAATACAAGAAGACGACGTATCCAGAATTACATCCACAATGAATACA
    230       240       250       260       270       280       290       300

         60        70        80        90       100       110       120
     CTGACCTGGCCATTCATCGGTGACATCAGTGACGTGAAGACTGACATCTTCCTGCGTAAGGACACTCAACGAGG
     |||||||||||| ||||||||||||||||||||||||||||||||||    ||||| ||||| ||||||||||||
     CCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGA---TCTCCATTCCGCGGTAACCGTATCATCTGGA
    310       320       330       340       350       360       370

        130       140       150       160       170       180       190
     AGACTGAGGTGATCTACTACCCAGACAACGTGTCAGTAGACCAAGTGATCCTCAGTAAGAACAACCTCCGA--
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     CTCTGATCGATATCAACGGTAAGACCAAACTGTATTCTTCGAATACAACATCCGTGAAGACATCTCTGAAT
    380       390       400       410       420       430       440

        200       210       220       230       240       250       260
     GCATGGACAACTAGACCTGCCTACC----CTAGTATCGACAGTGAAGTGAGAGATC--CTGCCCAGGGGAGAA
     |||||||||||||||||||| |||||    |||||||||||||||||||||||||     ||||||||||||||
     ACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAAATAATCTAAAATCTACATCACGGTAAAC
    450       460       470       480       490       500       510

        270       280       290       300       310       320
     TCAAGTCT----------TCTACGACAACCGTACCCAGAACGTGAGCTGGACTACCTCGACTACTCCTACTACCTAG
     |||||||          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     TGGAATCTAATACCGACATCAAAGACATCCGTGAGCTTATCGCTAAC--GGTGAAATCAT-CTTCAAACTGG
    520       530       540       550       560       570       580

        330       340       350       360       370       380
     AGTCTCAGAAGCTGAGT-----GACAACGTGGAGGACTTCACTTTCACGGTTCA-ATCGAGGAGGCTCTGG
     |||||||||||||||||     |||| |||||||||||||||||||| |||| |||||||||||||||||
     ACGGTGACATCGATCGTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCCAACACCGAACTGTCTCAGT
    590       600       610       620       630       640       650

        390       400       410       420       430       440       450
     ACAACAGTGCAAAGGTGAC-ACTTACTTCCCTACCTGGCTAACAAGGTGAATCCGGGTGTGCAAGGTGGT
     |||||||||| |||||||||   |||||||||||||||| ||||||||||||||||||||||||||||||
     CCAATATCGAAGAACGTACAAGATCTACTCCGATTACTCCGAATACCTGAAAGACTTCTGG--------GGT
    660       670       680       690       700       710

        460       470       480       490       500       510       520       530
     CTGTTCCTGATGTGGGCAAACCACGTGGTTGAGGACTTCACTACCAACATCCTGCGTAAGGACACACTGGAC
     ||||||| ||||||||| |||| |||||||||| ||||||||||||||||||||||||||||||||||||||
     AATCCGCTGATGTACAACAAGAATACTATATGTTCAATGCTGGTACAAGAACTCTTACATCAAACTGAAG
    720       730       740       750       760       770       780

        540       550       560       570       580       590
     AAGATCTCAGATGTGTCAGCTATCATCCCC-----CTACATCGGACCCGCACTGAACAT-CTCCAACT----
     |||| ||||| || ||||||||||||||         |||||||||| |||||||||| |||||||
     AAAGACTCTCCGGTTGTGAAAACTCGTTCCAAATCAACAAACTACAACCAGAACTCTAAATACCACCGC
    790       800       810       820       830       840       850       860

        600       610       620       630       640       650       660
     ---CTGTGCGTCGTGAAACTTCACTGAGGCATTCCACTGAGCTGATCTCTGGTGTCACCATCCTGCTGAGGCATTCC
    790
```

```
GAACACTTCCAACTCTGTGCGTCGTCGAGAAACTTC----ACTGAGGCATTCGCAGTCACTGGTCGTGTCACCATCC
| ||  |||||  ||||    ||  |  |||||| |       ||  |||| ||| | ||||    ||| |||   |
AATCAGATCCA--GCTGTTCAATCTGGAATCTTCCAAAATCGAAGTATCCTGAAAGAATGCTATC-GTATAC
 170        180        190        200        210        220        230

650        660        670        680        690        700        710
TGCTTGGAGGCATTCCCTGAGTTCAACCTGCTCTGGGTGCAT-TCGTGATCTCACAGTAGGTTCCAGGAG
 |||  |  ||   || |||  |||  || | ||| |||  ||  ||| | |  |||| |  |||||||||
AACTCTATG--TACGAAAACTTCTCCA-CCTCCTTGGATCCGTATCCCGAAATACTTCAACTCCATCTCT
 240        250        260        270        280        290        300

720        730        740        750        760        770        780
CGAAACGAGATCATCAAGACCATCGACAACTCTGGAGCAGGAATCAAGAGATGAAGGACTCCTACGACGT
| |  ||  |  |||| || ||||| ||  | |||| || |||  ||| |||  |  ||| |||||||
CTGAAC---AATGAATACACCATCATCAACTGCATGA--AAACAATTCTGGTTGGAAAGTATCCTGAACT
 310        320        330        340        350        360        370

810        820        830        840        850        860        870
GGTTGTCCAGGATCATCACCCAGTTCAACAACATCTCCTACGATGTACGACTCCCTGAACTACCAGGCAG
| | ||||| |  ||||||  |||  |||  ||  |   ||   | |  || | |||    |||||| |
TCTACAACACCATCCAGATCAAAGAATACGAACAGCCGACCTACCTG------------ACATCCTACCAGA
 790        800        810        820        830        840        850

880        890        900        910        920        930        940
GTGCAATCAAGGCTAAGATCGAGTACTCCGGAAGCGACAAGAGGAACATCAAGAGCC
| | |||||| |  |||  |||| ||| ||  | || |  || | | ||||||  |
TGTACGACTCCCTGAACTACCAGGCAGCTGCAATCAAGGCTAAGATCTCGGAGTACTCCG
 850        860        870        880        890        900        920

950        960        970        980        990        1000
AGGTTGAGAACCTGAAGAACAGTCTGGACGTCAAGATCTCCGGAGCCAATGAACACATCAACAGTTCATCC
| |||  |||  | ||||||| |  |||||| ||| || |||| |  |||| | |   |||   || | |
GAAGCGACAAGAGGAACATCAAGAGCCAGGTTGAGAACCTGAAGAACAGTCTGGACGTCAAGATCTCGGAGG
 930        940        950        960        970        980        990

1030        1040        1050        1060
GAGAGTGCTCCGTCACCTACCGTTCAAGGAACATGTCGCCTAAGGTGCATCGAGAAGCTGAACGAGTTCGACC
|  |   || |  ||||||||| | | || ||||| | |  |  ||  |  ||| ||||| ||   ||| ||
AAATCTCAACGGCCGTCGATC---GACCAGAAACCGATCTCCAATCTG---GGTAACATCCACGTT
 520        530        540        550        560        570        580

ACAAATACGTTGA
||  |||  | |
ACAAATACGTTGA
 800
```

```
 370        380    X   390        400        410        420        430
CACCGCGTTCAATCGAGGAGGCGTCGGACAACGGTACACTTACTTCCCTACCCTGGCTAACAA
|||||                  | |||  | |||   || |   ||  |  |  |||| |||
CTCGAGGCCATGGCTGCTGCCGTCGTCCAGATCATCATCAAGACACAT
        X      10         20         30         40         50
                                                              440        450
                                                              GGTGAATGCCGGTGTGCAAGGTGGTCGTTCCTGATCGTTGGGCAAACGACGTGGTTGAGGACTTCACTACCAA
                                                               440        450        460        470        480        490        500
```

```
CATCAATACCTCCAT--------CCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTA
   60                              70        80        90       100       110

510       520       530       540       550       560       570
CATCCTGCGCTAAGGACACACTGGACAAGATCTTCAGATGTGTCAGCTATCATCCCCTACATCGGACCCGCACT
|--||--||--|||--||--|                 ||--|||--|        ||--||--||
C--GCTTCCAAAATCAACATCGG---------------TTCTAAAGTTAACTTC-----GATCCGATCGACAAG
   120       130                        140              150             160

580       590       600       610       620       630       640
GAACATCTCCAACTCTGTGCGTCCTGGAAACTTC----ACTGAGGCCATTCCAGTTCACTCGTGTCACCATCC
|--|||--|||--||||| |||||                ||--|||--|||||--|||--||||--|
AATCAGATCCA--GCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATC-GTATAC
170          180       190       200       210       220       230

650       660       670       680       690       700       710
TGCTGGAGGCATTCCCTGAGTTCACAATCCCTGCTCTGGGTGCAT-TCGTGATCTACAGTAAGGTCCAGGAG
|||--|||--|         |||--||||--|||--||||--|||||
AACTCTATG--TACGAAAACTTCTCCA-CCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCT
240             250       260       270       280       290       300

720       730       740       750       760       770       780
CGAAACGAGATCATCAAGACCATCGACAACTGTCTGGAGCAGAGGATCAAGAGGACTCCTACGAG
|--|||--|         |||--||||--|||--||||--|||--|||||
CTGAAC---AATGAATACACCATCATCAACTGCATGGA--AAACAATTCTGTTGGAAAGTATCCTGAACT
310          320       330       340       350       360       370

790       800       810       820       830       840       850
TGGATGATGGGAACGTGGTTGTCCAGGATCATCACCCAGTTCAACA----------ACATCTCCTACCCAGA
|--|||--|||--||||--|||--|||||--|         ||--|||
ACGGTGAAAATCATCTGCAGGACACTCGCAGGACACTCGCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGA
380       390       400       410       420       430       440

860       870       880       890       900       910       920
TGTACGACTCCCTGAACTACCAGGCAGGTGCAATCAAGGCTAAGATCGAACCTGGAGTACAAGAAGTACTCCG
|||--|||--||||--|||--|||--||||--|         ||||
TGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCA
450       460       470       480       490       500       510

930       940       950       960       970       980       990
GAAGCGACAAGGAGAACATCAAGAGAACCTGAGAACCTGAAGAACCAGCAGTCTGGACGTCAAGATCTCGGAGG
|--|||--||--|         |||--|||--|||--||||--|||--|||--|
AAATCTACATCAACGGCCGTGTGATC---GACCAGAAACCGATCTCCAATCTG--GGTAACATCCACGCTT
520          530       540       550       560       570       580

1000      1010      1020      1030      1040      1050      1060
CAATGAACAACATCAACAAGTTCATCGGACGGTTGCGTGACAGTG--CTCCGTCACCTACCTGTTCAAGAACATGCTGCCTA
|--|||--|||--|||--|         ||||--|||--|
CTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGGTACATCTGGATCAAAATACTTCAAATC
590          600       610       620       630       640       650

1070      1080      1090      1100      1110      1120      1130
AGGTCATCCACGAGCTGAACGAGTTGACAAGCTGACAGCTGAAGGCAAGGTAAACAACCTGATCGACTCCCATA
|--|||--|||||                 |||--|||--|||||
TGTTCGACAAGAACTGAA------CGAAAAAGAAATCGAAGGTCAAAGGCAAAGGTAAACAACCGTACTACGTA
660          670       680       690       700       710       720

1140      1150      1160      1170      1180      1190      1200
ACATCATCCTGGTCGGTGAGGTGACGTGACAGCTGACAAGGTAAACAACAACAGCTTCCAGAACTAA
|--|||--|||--||||--|||                    |||||
TCCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAACTACTACCGTACTACATGCTGAATCGTGAATCGTGAATCGTGAATACTCTGGTA
730       740       750       760       770       780       790

ACAAATACGTTGA
800
```

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O| |O   IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-23-inv.res made by bobryen on Thu 7 Nov 102 14:48:11-PST.

Query sequence being compared:US-09-910-186A-23' (1-1200)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-23' (1-1200) with:
   File :US08123975A.seq   *complement*

```
100-|

N  -|
50-|
U  -|
M  -|
B  -|
E  -|
R  -|

O  -|
F  10-|

S  -|
E  5-|
E  -|                      *
Q  -|
U  -|
E  -|                                          *
N  -|
C  -|
E  -|
S  0-|------------------------------------------------------
        16   24   32   41   49   57   65   73
SCORE 0  -8                         0              --   --   --
STDEV    -1                                                73
                                                           1

        PARAMETERS
Similarity matrix    Unitary     K-tuple            4
Mismatch penalty     1           Joining penalty   30
Gap penalty          5.00        Window size      500
Gap size penalty     0.33
Cutoff score         0
Randomization group  0

        SEARCH STATISTICS
Scores:    Mean    Median    Standard Deviation
           58      29        25.98

Times:     CPU                Total Elapsed
           00:00:00.00        00:00:00.00

Number of residues:          4027
Number of sequences searched:   3
Number of scores above cutoff:  3
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
                                                                        Init.  Opt.
Sequence Name    Description                                Length Score Score Sig. Frame
---------------  -----------------------------------------  ------ ----- ----- ----  -----
1. US-08-123-975A-4  Sequence 4, Application U               1338    73   449  0.58    0
2. US-08-123-975A-1  Sequence 1, Application U               1338    73   449  0.58    0
                     **** 1 standard deviation below mean ****
3. US-08-123-975A-6  Sequence 6, Application U               1351    28   440  -1.15   0
```

1. US-09-910-186A-23' (1-1200)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

```
Initial Score     =   73   Optimized Score  =  449   Significance =  0.58
Residue Identity  =  428   Matches          =  527   Mismatches   =  653
Gaps              =    0   Conservative Substitutions = 62   Conservative Substitutions =    0
```

```
                      X         10        20        30        40        50
            TTAGTTCTTGGAAGCTGTTGTTTACCTTTGCCTTCAGCTTGTCGCGACCTCACCG
            |||||||  ||| |||| ||  ||| |||||||||| || ||| |||| |||||||
CTGCTGTCTACCTTCACTCAGTACATCAAGAACATCATTGGCTTCCATCCTGAACCTGCGCTACGAATCC
  20        30        40        50        60        70        80

            ACCAGGATGATGTTATGGGAGTCGATCAGCTTGATCAGTTGGTTCGGTTCGGTCGAACTCGTTCAGC
            |||  || | ||  ||  ||||||| |||||| |||||| || |||||  ||  ||  ||||| |||
AATCACCTGAT-CGACCTGTCTCGCT-ACGGTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGA
  90        100       110       120       130       140       150

                 130       140       150       160       170       180       190
            TCGTCGATGACCTTAGGCAGCCAGCATGT--TCTTGAACAGGTAGGTGACGGACCACTCTCGGATGAGAACTTGTTG
            |||| ||| || | |||  |||||| ||    ||||||  ||||  || ||  ||  |||  |||| ||||  ||||
TCGACAAGATCAGATCCAGCTGTTCAATCTTGGAATCTTCCAAAATCGAGTTATC-CTGAAGAATGCTATC
160        170       180       190       200       210       220       230

                 200       210       220       230       240       250       260
            ATGTTGTTCATTGCCTCCGAGATCTTGACGGTCCAGACTGTCTTCAGGTTCTCAACCTGGCTCTTGATGTTC
            ||| || ||||   ||||||  |||  |||||  |||| |||| |||  ||  |  ||||| || |||| |||
GTATACAACTCTATGTACGAAAACTTCTCCACCTCTTCGGATCCGTATCCCGGAAATACTTCAACTCCATC
240        250       260       270       280       290       300

                 270       280       290       300       310       320       330
            TCCTTGTCGCTTCCGGAGTACTTCTTGTCTGTACTCCAGGTCGATCTTAGCCTTGGAAAGTATCTCTGAACTA
            ||| | ||||  | |  || | |  ||| ||  |||| |||||||  |||| ||||  |||||||||||||| ||
TCTCTGAACAATGAATACACCCATCCATCACCAACTGCATCGAAAAC-AATTCTCGTTGGAAAGTATCTCTGAACTA
310        320       330       340       350       360       370

            340       350       360       370       380       390       400
            AGGGAGTCGTACATCTG-----GTAGGAGATGTTGTTGAACTGGGTGATGATCCTGGACAACCACGTTCCC
            |  ||| || |||| ||     || |||| |||| ||||||||| || ||||| ||||  ||  ||  ||||
CGG--TGAAATCATCTGGACTCGCGACACGCACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAG
380        390       400       410       420       430       440

            410       420       430       440       450       460       470
            ATCATCCACCTCGTAGGAGTCCTCCCATCTCTTGATCCTCCAGACAGTTGTCGATGGTCTTGATGATC
            ||| ||| |  |||||| ||||| ||| ||||| |||  |||| || | |  |  || ||||||||||
ATGATCAACACATCTCTGCTACTACAATCGCTGGACTTCGTTACC--ATCACCAACAATCGTC-TGAATAAC
450        460       470       480       490       500       510

            480       490       500       510       520       530       540
            TCGTTTCGCTCCTGGACCTTACTGTAGATCGAATGCACCCAGACGAGCAGGGATTGTGAACTCAGGGAATGCC
            || | |||| ||| ||||| || |  ||  ||| | ||||| || |  || ||  |  ||| ||  ||  |||
TCCAAAATCTACATCACGGGCCGTCGTTGACCAGAAACGATCTCCAATCTGGTAACATCCACCGCCTTCT
520        530       540       550       560       570       580

            550       560       570       580       590       600       610
            TCCAGAGGAGGTGACCAGTGACTGGCGAATGCCTCAGTGAAGTTCCACGACGCCACCAGAGTTGGAGATG
            ||| | ||||  |  || || | |  |  ||  |||  |||||||  || |   ||  ||  |||| ||||
AATAACATCATGTTCAAACTGGACGGTTGTGACTCACCGTCACTCTGGATCATGTCAAATACTTCAATCTG
590        600       610       620       630       640       650

            620       630       640       650       660       670       680       690
            TTCAGTCGCGGGTTCCGATGTAGGGGATGATAGCTGACACATCTGAGATCTTGTCC-AGTGTGTCCTTACCCAG
            ||||                                                   |  |||||||  ||||| ||
620        630       640       650       660       670       680       690
```

2. US-09-910-186A-23' (1-1200)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score	=	73	Optimized Score =	449	Significance =	0.58
Residue Identity	=	42%	Matches =	428	Mismatches =	527
Gaps	=		Conservative Substitutions =	62		653 / 0

```
ACCAAT---GCTTCTCAGGCTGGTGGTGTAGAAAGACATCTGTCTGCTCTGGAAATCCCGGACGTTGGTAAATCTG
1020          1030        1040        1050        1060        1070        1080
          | | | |       | | |       | | | |       | | | |       | | |       | | | |
1030   GATCA-CTTGGTCTACTGACA-CGTTGTCTGGTAGATGCACCTCAGTCTCCTCGTTGATGTCCTTACGC
1090        1100        1110        1120        1130        1140

1100   TCTCAGGTAGTTGTAATGAAATCAAGAACGACCAGGGTATCCACTCAACAAATGCAAAATGA----ATCTGC
       1090        1100        1110        1120        1130        1140        1150

1100   AGGAAGAGATGTCAGTTCTCACGTCACTGATGTCACCGATGAATGGCAGGTCAGTGTT----CTTCACCAGCAG
       1110        1120        1130        1140        1150        1160

       AGGACAA---CAATGGTAACGATATCGGTTTCATCGGTTTCAACAATATCGCTAAACTGGTTG
       1160        1170        1180        1190        1200        1210        1220

       1170        1180        1190
       CTCTTCTACAG--TCAAGGGTCTTGTTGTTGTACAGGGACAT
                                    X
       CTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCCGACCTCGGGTTGCTCTTG
       1230        1240        1250        1260        1270
```

3. US-09-910-186A-23' (1-1200)
    US-08-123-975A-6 Sequence 6, Application US/08123975A

```
Initial Score  =    28   Optimized Score  =   440   Significance =   -1.15
Residue Identity =  40%   Matches         =   539   Mismatches   =    647
Gaps           =   154   Conservative Substitutions  =           0
```

```
X  10          20          30          40          50          60          70
   TTAGTTGTGAAGCTGTTGTTTACCTTTGCCTTCAGCTGTGTCGACTCACCGACCAGGATGATGTTATGGGA
     | | | | |     | | |       | |       | | | |     | | |       | | | |
   ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCCTGAACCTGCGTTACAAAGAC
X   10          20          30          40          50          60
```

```
 80          90          100         110         120         130         140
 GTCGATCAGGTGATCAGCTTTGCCTTGGTGTTTCGGTCGGAACTGTTCAGCTCGTCGATGACCTTA--GGC
   | | |   | | | |       | | | |     | | |       | | | |       | |
 AACAATCTGATCGATCCTGGACTTCTCTGTTCCGTCGTCGCTAAAGTTGAA---GTATACGACGGTGTTGAACTGAATGAC
 70          80          90          100         110         120         130
```

```
 150         160         170         180         190         200
 AGCATGTTCTTGAACAGGTAGGTAGGTGACGGAGCACTCTCGGATGAACTTGTT-------GATGTVGTTCA
   | |   | | | |       | | | |     | | |   | | | |     | | | |
 AAGACCAGTTCAAACTGGTTTCCGCTAACTGCTCTAAGAT--CCGTGTTACTCAGAATCAGAACAATCATCT
 140         150         160         170         180         190         200
```

```
 210         220         230         240         250         260         270
 TTGCCTCCGAGACTTGACGTACCCAGACTGTTCTTCAGGTTCTCAACCTGGCCTTGATGTTCTCC---TTGT
   | | | |   | | | |     | | | |     | | |       | | | |       | |
 TCAACTCCGTATTCCTGGACTTCTCTGTTCCTCTCGAATCCGTATCCCGAAATACAAGAACGACGACGGTATCC
 210         220         230         240         250         260         270
```

```
 280         290         300         310         320         330         340
 CGCTTCCGGAGTACTTCTTGTACTGTGTAGCCAGGTGACGATCTTAGCCTTGATGCACCTGGTGAGTTC------
   | | | |   | | | |     | | |     | | | |       | | | |     | | | |
 AGAATTACATCACCACAATGAATACACCACATCATCAACTGCATGAAGAATAAACTCTGGTTGGAGATCTCCATCC
 280         290         300         310         320         330         340
```

```
 350         360         370         380         390         400
 -AGGGAGTCGTA-CATCTGGTAGGAGATGTTGTTGAACTGGGTGATGATCCTGGCGTAAGCGTAAGAACCAGTTCCCATCA
   | | | |   | | | |       | | |       | | | |     | | | |
 GCGGTAACCGTATCATCTGGTGATCGAATCTGGACTTCGTTCGAATCGTATTCTTCGAATACAACA
 350         360         370         380         390         400         420
```

```
 410         420         430         440         450         460
 TCC------ACTCGTAGGAGGTCCTTCCATCTCTTGATCTC------TGCTTACCATCACCAATTACCTGATGGGTC
   | | |   | | | |       | | |       | | |     | | | |
 TCCGTGAAGACAATCCTGAATAACATACACTACATCGCTCGTCGGTTCTTCGTTACCATCACCAATAACTGCTA
 430         440         450         460         470         480         490
```

```
 470         480         490         500         510         520         530
 TTGAATGAATCCGTTTCGCTCCTGGACCTTACTGTAGATCACGAATGCACGGAGCACCCAGAGCGCAGGGGATTGTGAACTCA
 350         360         370         380         390         500        510        520        530
```

Page 2 (second half / right column):

```
AAATACTATCAACGGTAAACTGGAATCTAATACCGACACTCAAAGACATCC-GTGAAGTTATCGCTAACGGT
500          510        520        530        540        550        560
          | | | | |     | | |       | | |       | | | |
540   GGGA-ATGCCTCCAGCAGGATGGTGACACCGGTGACTGCGAATGCCCAG--TGAAGT-------TTC
      550        560        570        580        590        600        610

570   GAATCATCTTCAAACTGGACGGTGACATCGATCCAGTTCATCTGGATGAAATACTTCTCCATCTTC
      580        590        600        610        620        630

600          610        620        630        640        650
CACGACGCCACAGAGT-------TGGAGATGTTCAGTGC-GGGTCCGATGTAGGGGATGAGAGCTGACACAT
                           | | | |     | | |       | | | |     | | | |
AACACCGGACTGTCAGTTCAGATCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGAC
640          650        660        670        680        690        700

660          670        680        690        700        710        720        730
CTGAGATCTTGTCGACGTGTCCTTACCCAGGATGTTGTAGTGAAGTCCT-CAACCACGTCGTTTGCCCAC
          | | |     | | | |       | | |     | | | |       | | | |
TTCTGGGGTAATCCGCCTGATGTACAACAAGAATACTATATGTTCAATGTTCAATGCTGTAACAAGAACTCTTACATC
710          720        730        740        750        760        770        780

740          750        760        770        780        790
ATCAGGAACAGA----CCACCTTGCACACCGGCATCCACCTTGTTAGCAGGTAGGCAGGTAGGTAAGTAGTGTA-
          | | |     | | | |       | | | |       | | |       | | |
AAACTGAAGAAGACTCTCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAATACATC
790          800        810        820        830        840        850

       800        810        820        830        840        850
-------CACCTTTGCACGTGTTGTCCAGCCTCCTGATTGAACGCGTGAAAGTGAAGTCTCCACGTT
          | | |     | | | |       | | | |       | | |
AACTACCGCGACCTGTACATCCGTGAAAAGTTCATCATCGTCGCAAATCAACTCAACTCAGTCCATCAATGAT
860          870        880        890        900        910        920

860                                          870        880        890
GTCA-----                                    CTCAGCTTCTGAGACTCTCAGGTAGTA---------GTAGGAG
   | | |                                       | | |     | | |       | | |
GACACGTACGTAAGAGCTAAAGAACGACTACACTCACCTACCTGGACTTCTTCAACCTGACTGAATCGAATGGCCTGTATACACC
930          940        950        960        970        980        990

       900        910        920        930        940        950        960
TTCAGGTAGTCCACGTTCTCGGGTACGGTGTCGTTCGTAGAAGAGACTTGATTCTCCCCTGGC-AGGATCTCCACTCTC
          | | |     | | | |       | | | |       | | |       | | |
TACAAGTACTTGACAAAGAAGAAGAAAAAGCTTTTCCTGGCTCCGATCTGTGATTCCGACGAACTCTACAAAC
1000         1010        1020        1030        1040        1050        1060

970          980        990        1000        1010        1020        1030
ACTGTCGGATACTAGGGTAGAGCCAGGTCAGTGTCC--ATGCTCGGAGGCTGGTGTTCTTACTGAGGATCACTGG
          | | |     | | | |       | | |       | | | |     | | | |
ACCATCAGATCAGAATACGACGAAGCAGCCGACCTACTTCCAGGTCTGCCAGTTCAAGAAGATGAAGAA
1070         1080        1090        1100        1110        1120        1130        1140

1040         1050        1060        1070        1080        1090        1100
TCTACTGACACGTTGTCTGGTAGGATCCAGTCTCCAGTCTCCGTTGATGTCCTTACGCAGGAGATGTCA
          | | |     | | | |       | | | |       | | |
TCTACTG--ACGAAATCGGTCGATCGGTATCCAACTGGTTCTACGGTATCGGTATTCGAAGAATACA
1150         1160        1170        1180        1190        1200        1210

1110         1120        1130
-GCTTCACGTCACTGATGATGTCACCGATGAATG-----------------
   | | |     | | | |
TTCTTCACCAGCAGCTCTCTCTACAGTCAGGGTCTTGTTGTTGTACAGGGACAT
1290         1300        1310        1320        1330 X        1340        1350
                                             X

1140         1150
-----------------GCAGGTCAGTG
AAGAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAGTTAAAACGGAGGTAAACCTACAAACCTGAAACTGGGTT
1220         1230        1240        1250        1260        1270        1280
```

```
> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-24.res made by bobryen on Thu 7 Nov 102 14:36:15-PST.

Query sequence being compared:US-09-910-186A-24 (1-399)
Number of sequences searched:          3
Number of scores above cutoff:         3

Results of the initial comparison of US-09-910-186A-24 (1-399) with:
      File : US08123975A.pep
```

```
100-
     |
   N |
   U 50-
   M  |
   B  |
   E  |
   R  |
      |
   O 10-
   F  |
      |
   S 5-
   E  |
   Q  |
   U  |              *
   E  |
   N  |
   C  |
   E  |                                                                      *
   S 0----|---|---|---|---|---|---|---|---|---|---|---|
          0  21  41  62  83 103 124 145 165 186
   SCORE  0  21  41  62  83 103 124 145 165 186
   STDEV  0               1       1
```

```
                PARAMETERS

Similarity matrix      PAM-150
Threshold level of sim.   16%
Mismatch penalty          1
Gap penalty             5.00
Gap size penalty        0.05
Cutoff score              1
Randomization group       0

              SEARCH STATISTICS

Scores:         Mean      Median    Standard Deviation
                 74         19            96.71

Times:          CPU                   Total Elapsed
            00:00:00.00               00:00:00.00

Number of residues:                1704
Number of sequences searched:         3
Number of scores above cutoff:        3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
Sequence Name      Description              Length Init. Opt. Sig. Frame
                                                   Score Score
------------------------------------------------------------------------
                        **** 1 standard deviation above mean ****
 1. US-08-123-975A-2  Sequence 2, Application U  850  186  263  1.16   0
                        **** 0 standard deviation from mean ****
 2. US-08-123-975A-3  Sequence 3, Application U  415   19  177 -0.57   0
 3. US-08-123-975A-5  Sequence 5, Application U  439   18  175 -0.58   0
```

```
1. US-09-910-186A-24 (1-399)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score   =  186   Optimized Score =  263   Significance = 1.16
Residue Identity =  34%  Matches         =  136   Mismatches   = 223
Gaps             =   1   Conservative Substitutions =   1        = 33

           10        20        30        40        50        60        70
   MSLYNKTLDCRELLVKNTDLPFIGDISDVKTDIFLRKDINEETEVIYPDNVSVDQVILSKNTSEHGQLDLL
                     ||||:||  |  :|   : ||||| |     :|    :||| ||
   APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSE
   X         10        20        30        40        50        60

           80        90       100       110       120       130       140
   YPSIDSESEILPGENQVFVDNRTQNVDYLNSYYYLESQKLSDNVEDFTFTRSIEEALDNSAKVYTYFP-TLA
            ||  :||:| |:| :  |   ::||  :|| : : :||| :   :||:   : :::||| ::
   NTESLTDFNVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYI
   70        80        90       100       110       120       130

          150       160       170       180       190       200       210
   NKVNAGVQGGLFLMWANDVVEDFTNILRKDTLDKISDVSAIIPYIGPALNISNSVRRGNFTEAFAVTGVTI
      :|||| | :: : |     ||  |   ||   :|     | || ||| : :::|| ||    |
   KTANKVVEAGLFAGWVKQIVNDFVIEANKSNYMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASI
   140       150       160       170       180       190       200

          220       230       240       250       260       270       280
   LLEAFPEFTIPALGAFVIYSKVQERNEIIKTIDNCLEQRIKRWKDSYEWMMGTWLSRIITQFNNISYQMYDS
    ::|||  || |      |||         ||||:: | ||| | |   || | : |  ||   : ||||
   LLEFIPELLIPVVGAFLLESYIIDKNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKA
   210       220       230       240       250       260       270       280

          290       300       310       320       330       340       350
   LNYQAGAIKAKIDLEYKKYSGSDKENIKSQVENLKNSLDVKISEAMNNINKFIRECSVTYLFKNMLPKVIDE
   |||||     | |  :||     | || :|||| ::|    || | :| |       | || ||||||||
   LNYQAQALEEIIKYRYNIYSEKEKSNNIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEK
   290       300       310       320       330       340       350

          360       370       380       390
   LNEFDRNTKAKLINLIDSHNIILVGEVDKLKAKVNNSFQN
    :|| ||||||  |||: |||::|| | :||: |:|:|||         X
   LLDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFN
   360       370       380       390       X       400      410
```

```
2. US-09-910-186A-24 (1-399)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score   =   19   Optimized Score =  177   Significance = -0.57
Residue Identity =   7%  Matches         =   30   Mismatches   = 342
Gaps             =   6   Conservative Substitutions =   6        = 22

           10        20        30        40        50        60        70
   X         MSLYNKTLDCRELLVKNTDLPFIGDISDVKTDIFLRKDINEETEVIYPDNVSVDQVILSKNTSEHGQLDLL
             ||
   RYESNHILDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKY
   X         10        20        30        40        50        60        70

           80        90       100       110       120       130       140
   YPSIDSESEILPGENQVFVDNRTQNVDYLNSYYYLESQKLSDNVEDFTFTRSIEEALDNSAKVYTYFPTLAN
    : ||                                              ||
   FNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI--NISDYINRWIFVTINN
   80        90       100       110       120       130       140
```

```
               150       160       170       180       190       200       210
KVNAGVQGGLFLMWANDVVEDFTNILRKDTLDKISDVSAIIPYIGPAL--NISNSVRRGNFTEAFAVTGVT
   :-|: :    |                           ||-     -   :    |::  :
RLNNSKIYINGRLIDQKPISNLGNIHASNIMFKLDGCRDTHRYIWTKYFNLFDKLNEKEIKDLYDNQSNS
   150       160       170       180       190       200       210

       220       230       240       250       260       270       280
ILLEAFPEFTIPALGAFVIYSKVQERNEIIKTIDNCLEQRIKRWKDSYEWMMGTWLSRIITQFNNISYQMYD
           :                        |-                   |
GILKDFWGDYLQYDKPYYMLNLYDPNKYV--DVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKK
   220       230       240       250       260       270       280

       290       300       310       320       330       340       350
SLNYQAGAIKAKIDLEYKKYSGSDKENIKSQVENLKNSLDVKISEAMNNINKFIRECSVTYLFKNMLPKVID
       ||                                :                |
YASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCK
   290       300       310       320       330       340       350

   360       370       380       390        X
ELNEFDRNTKAKLINLIDSHNIILVGEVDKLKAKVNNSFQN
   :-||-  ||
MNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRPLGCSWEFIPVDDGWGERPL
   360       370       380       390    X 400       410

3.  US-09-910-186A-24 (1-399)
    US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =      18   Optimized Score    =     175   Significance   =   -0.58
Residue Identity =     10%   Matches            =      45   Mismatches     =    325
Gaps             =      29   Conservative Substitutions    =      26

         X        10        20        30        40        50        60        70
MSLYNKTLDCRELLVKNTLDPFIGDISDVKTDIFLRKDINEETEVIYYPDNVSVDQVILSKNTSEHGQLDLL
   ||-|:   |                               :        :   |
FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVIDGVELNDKNQFKLITSSANSKIRVTQNQNIIFNSVFL
   X        10        20        30        40        50        60        70

        80        90       100       110       120       130       140
YPSIDSESEILPGENQVFVDNRTQNVDYLNSYYLESQKLSDNVEDFTFTRSIEEALDNSAKVYTYFPTLAN
   :-|:                                |:   :          |
DFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLI--DINGKTKSVFFEYNIRE
        80        90       100       110       120       130       140

         150       160       170       180       190       200
KVNAGVQGGLFLMWANDVVEDFTNILRKDTLDKISDVSAIIPYIGPALNISNSVRRGNFT-----------
   :-|: :    |                        ||:||: |
DISEYINRWFFVTIINNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIRTQFIWMKYFSIFNTE
   150       160       170       180       190       200       210

        210       220       230       240       250       260       270
------EAFAVTGVTILLEAFPEFTIPALGAFVIYSKVQERNEIIKTIDNCLEQRIKRWKDSYEWMMGTWL
       : : :     |  :                      |
LSQSNIEERYKIQSYSEYLKDFWGGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYINQNSKYINYR
   220       230       240       250       260       270       280

        280       290       300       310       320       330
S-----RIITQFNNISYQMYDSLNYQAGAIKAKIDLEYKKYSGSDKENIKSQVENLKNSLDVKISEAMNNIN
   :-:                               |-
DLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQ
   290       300       310       320       330       340       350

   340       350       360       370       380       390        X
KFIRECSVTYLFKNMLPKVIDELNEFDRNTKAKLIN---LIDSHNIILVGEVDKLKAKVNNSFQN
   ::-||-  ||           :
IKEYDEQPTYSCQLLFKKDEESTDEIGLLGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQ
   360       370       380       390       400       410    420 X

FIPKDEGWTE
430
```

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O|/O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-25.res made by bobryen on Thu 7 Nov 102 14:48:41-PST.

Query sequence being compared:US-09-910-186A-25 (1-1161)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-25 (1-1161) with
       File : US08123975A.seq

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-6 Sequence 6, Application U	1351	165	453	1.15	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-4 Sequence 4, Application U	1338	126	443	-0.58	0
3. US-08-123-975A-1 Sequence 1, Application U	1338	126	443	-0.58	0

1. US-09-910-186A-25 (1-1161)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score   = 165   Optimized Score   = 453   Significance =   1.15
Residue Identity = 43%   Matches   = 528   Mismatches   =   610
Gaps   =   Conservative Substitutions =   88

```
            10        20        30        40        50        60        70
X   ATGGCCAACTCCCGTGACGACTCCACCTGCATCAAGGTCAAGAACACAGACTGCCATACGTTGCCGACAA-
    ||||||||||||||||||||||||||||||||||||| || |  ||| ||||  ||| || |||| ||||
X   ATGGCTTCAACAAATACAATTCCGAAATCCTGAACATATCATCCTGAACCTGCGTTACAAAGACAACAAT
X   10        20        30        40        50        60        70

           80        90       100       110       120       130
    GGACTCCATCCCCAGG---AGATCTTCGAGAACAAGATCATCACCGACGCAGACC--AACGTTCAAAACTAC
    || ||||| | ||||    ||||||| || ||||||   || ||  |||| ||    |||| |||| || |
    CTGATCGATCTGTCTGGTACGGTGCTAAAGTGAAGTTGAAGTATACGACGGTGTTGAACTGAATGACAAGAACCAG
           80        90       100       110       120       130       140

          140       150       160       170       180       190       200
    TCCGACAAGTTCTCTTGGACGAGTC---CATCCTGGACGGTCCAGGTCCCAATCAACCCAGAGATCGTCGAC
    |||||   |||| || |||||||||   |||| ||| |||| || ||  ||||||  | ||||  ||||||
    TTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTAAGATCCTGGTTACTCGTGGTCAGAAGCATCCTTCAACTCCGTA
          150       160       170       180       190       200       210

          210       220       230       240       250       260       270
    CCACTGTTGCCAAACGTCAACATGGAGCCATTGAACTTGACCTGCCAGGTGAGGAGTCGTCTTCTACGACGACATC
    |||| |  |||| || | || |||  || || || || || ||||  |||| || ||  | |||  ||||||
    TTCCTGGACTTCTCGTTTCCTTCTGATCCGTATCCCGAAATCAACAGAGACGACGTATCCAGAATTACATC
          220       230       240       250       260       270       280

          280       290       300       310       320       330       340       350
    ACCAAGTACGTCGACTACTTGAACTCCTACTACTGGAGTCTCAAAGTTGTCTAACAACGTCGAGAAC
    |     |  ||  |||| || |  | || |||| ||| || ||||||| || ||  |||| || |||
    CACAATGAATACACCATCAACTGCATGAAGAATAACTCTGGTTGGACAAGATCCCATCCGCGGTAACCGT
    290       300       310       320       330       340       350       360

          360       370       380       390       400       410       420
    ATCACCTTGACCACCTCCGTCGAGGAGCCTTGGGTTACTCTAACAAGATC---TACACCTTCTTGCCATCC
    | ||||||   | || ||  |||  ||| ||  || ||| ||  ||||     ||||||  |||||||
    ATCATCTGGACTCTGATCGATATCAAGGTAAGCGTAAGGTAAGACCAAATCGTATTCTTCGAATACAACATCCGTGAGAGC
          370       380       390       400       410       420       430

          430       440       450       460       470       480       490
    TTGGCTGAGAAGGTTAACAAGGGGTGTTCAAGGTGGTTTGTTCCTGAACTGGTTGGCCAACGAGGTCGTCGAGGAC
    | ||| ||   | | ||  ||   || || |  | |||  |  |||||  | || ||||| | || ||||  ||
    ATCTCTGAATACATCAA--------TCGCTGG-TTCTTCGTTACCATCCAATAACCTGAACAATG--
    440                         450       460       470       480       490

          500       510       520       530       540       550       560
    TTCACCACCAACATCATGAAGAAGGACACCCTGGACAAGAGATCCGGACGGTCTCCGTCATCATCCCATACATC
    ||   || |     || ||  |||| || ||   ||||  ||  || |  |||||| ||||  || ||||
    ------CTAAAATCTACATCACGTAAACTGGAATCTAATACCGACATCAAAAGACACATCCGTGAAGTTATC
    500       510       520       530       540       550

          570       580       590       600       610       620       630
    GGTCCAGCCTTGAACATC-GGTAACTCCGCCCTGAGAGAGGTAACTTCAACCAGGCCTTCGGCCACCGCCGGTCGT
    || ||||||| |||| |  ||||| ||| || ||    |     ||||||| |||  ||||||  |||  |||||
    GCTAACGGTGAAATCATCTCAAACTGACACGGTGACATCGATCGT-ACCCAGTTCATTCTGATGAGAAATACTT
    560       570       580       590       600       610       620

          640       650       660       670       680       690       700
    CGCCCTTCCTGCTGGAGGGTTTCCACCTTCACCATCCCAGCCTGGGTGTCTTCACCTTCACCTTCTCTACTTCCCAT
```

```
              |||||  |  |||||| ||| ||||| |||       ||      ||||||||
       ------ACGAGACCAACGTTCAAAACTACTCCGACAAGTTCTCTTGACGAGTCCATCCTCTGGACGGTC
       AAGTTAACTTCGATCCGATCGCAAGAATCAGAGAACTCAGCTGTTCAATCTGAAATCTTCCAAAATCGAATCC-
          150           160           170           180           190           200           210

       180           190           200           210           220           230           240           250
       AGGTCCCAATCAACCCAGAGATGCTGCGACCCACGTGTGCCAAACGTCAACATGGAGCCAATTGAACCTGCCAG
       ||| |||    ||||| |   | ||| |||  | ||| || ||||||||||||| ||||  |  ||||
       --ATCCTGAAGAATGCTATCGTATACAACTCATGTACGAACAGTTCCA---CCTCCTTCTCTGGATCCGTA
              220           230           240           250           260           270

       260           270           280           290           300           310           320
       GTGAGGAGATCGTCTTCTACGACGACACACCACCATCTCTCTGAACAATGAATACACCATCATCACTCGTTGGAGT
       ||| ||| |||   |||||||||||  |  ||||| |||||||||||||||||||||||||||||||||||||| |
       GAAGGAGTCCTACCAGTGACTGGATGG--TTTCCAACTG--GCTGTCCAGAATCACCACCCAATTCAACCACATC-
              780           790           800           810           820           830           840
```

(sequence alignment continues)

```
2.  US-09-910-186A-25 (1-1161)
    US-08-123-975A-4 Sequence 4, Application US/08123975A

    Initial Score       =    126    Optimized Score       =    443    Significance  =  -0.58
    Residue Identity    =    41%    Matches               =    546    Mismatches    =    600
    Gaps                =    159    Conservative Substitutions  =    159

         X         10        20        30        40        50
    ATGGCCAACTCCCGTGACGACTCCACCTGCATCAAGGTCAAGAACAACAGAC
    ||  ||||  ||||||||||||||||||||||||||| ||| ||||||||
    CTCGAGGCCATGGCTCGTCTGCTCTACCTTCACTGAATACATCAAGAACAAGAACATCA---TCAATACCTCCATCC
         10        20        30        40        50        60
```

```
AGGCCTTGGGTACTCTAACAGATCTACACCT----TCCTGCCATC------CTTGGCTGTGAGAAGGTTA
      ||||||     ||  | ||||||  |||      ||  |||          |||    ||||||
TTGTATTCAAATACTCTCAGATGATCAACATCTGACTACAATCGTCTGGATCTTCGTTACCATCACCA
              430          440          450          460          470          480          490

                     440          450          460          470          480          490          500
ACAAGGGTGTTCAAGCTGGTTGTTCCTGAACTGGGCCAAGCAGGTGTCGAACTTCACCACCACCATCA
      | |     |||||||||   ||   ||||   |||  ||||||  | | ||||||||   |||||
ACAATCGTCTGAATAAACTCCAAAATCTACATCAACGGCGTCGATCTGACCAGAAACCGATCTCCAATCTGG
       500          510          520          530          540          550          560

       510          520          530          540          550          560          570
TGAAGAAGGACACCCTGGACAAGATC----TCCGACGTCTCCATCATCCCATCAATCGTCCAGC----
  |||    |  | || ||||      |||        |||||||  |||||  ||||   |||
GTAACATCCACGCTTCTAATAACATGTTCAAACTGCCAACTTCACACTTCACCGTACACTCTCTGA
       570          580          590          600          610          620          630

                    580          590          600          610          620          630
----CTTGAACATCGTAACCTCCGCCCTGAGAGGTAACTTCAAC-CAGGCCTTGCGCCACGCGGT-
        ||||||  ||  | ||||||     |||||||||||       ||||     ||||||
TCAAATACTTCAATCTGTTCGACAAGAAACTGAACGAACAACCAGTACGT
       640          650          660          670          680          690          700          710

             640          650          660          670          680
------GTCCCT----TCCTGCTGGAGGGTTTCCC------------AGAGTTCCACATCCCACCCCTGG
         | |        ||||||||||   |||                |||||||||||||||| |||
ATTCTGGTATCCTGGAAAGACTTCTGGGGTGACTCTGGGTGACTACTCCGCAGTACGACAAACCGTACTACGCTGTCT
       720          730          740          750          760          770          780
```

```
3. US-09-910-186A-25 (1-1161)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =  126     Optimized Score      =  443     Significance  =  -0.58
Matches           =  41%     Matches              =  600     Mismatches    =  546
Residue Identity  =  41%     Conservative Substitutions  =  159     Gaps  =  0
```

```
                                     x              10           20           30           40           50
                                     ATGGCCAACTCCGTGACGACTCCACCTGCTCGCTGTCTTCACTGAAGAACAACAGAC
                                          |||  || |||||| |||||||       ||||||||||  |||||||||
CTCCAGCCATGGCTCGTCGTGCTTCCCTGACGTCTCTGCTGACTGAAGAACATCA--TCAATACCTCCATCC
         10           20           30           40           50           60
```

(alignment continues — dense nucleotide sequence data)

Thu Nov 7 14:52:39 2002

```
|  ||||||  |||||  ||| | |  |
AGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGG
    1290      1300      1310      1320      1330
```

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> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-25-inv.res made by bobryen on Thu 7 Nov 102 14:48:57-PST.

Query sequence being compared:US-09-910-186A-25' (1-1161)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

Results of the initial comparison of US-09-910-186A-25' (1-1161) with:
    File :US08123975A.seq                                    complement
```

```
                                                             Init.  Opt.
Sequence Name   Description                           Length Score  Score  Sig.  Frame
-------------   -----------                           ------ -----  -----  ----  -----
  1. US-08-123-975A-4 Sequence 4, Application U        1338   46    206    0.62    0
  2. US-08-123-975A-1 Sequence 1, Application U        1338   46    206    0.62    0
        **** 1 standard deviation below mean ****
  3. US-08-123-975A-6 Sequence 6, Application U        1351   32    246   -1.11    0
```

```
1. US-09-910-186A-25' (1-1161)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

   Initial Score     =  46   Optimized Score       =  206   Significance  =  0.62
   Residue Identity  =  39%  Matches               =  236   Mismatches    =  336
   Gaps              =       Conservative Substitutions  =  26   Gaps    =  0
```

```
     560       570       580       590       600       610       620       630
ACCTCTCAGGGCGGGAGTTACCGATGTTCAAGGCTGGACCGATGTATGGAGATGATGACCGAGCCGGAGAT
                           CTCGAGCCATGGCCTCGTCCTGCTGTCT--ACCTTCACTGAATACATCAAGAA
                           ||||||||||||||||||||||||||| |    ||||||||  ||||||  |||
                                   x       10        20        30        40

     640       650       660       670       680       690       700
CTTGTCCAGGGTGTCCTTCTTCATGAGTTGCTGGTGTGGAAGYCCTGCAGAGTCCTGCCCAGTTCAGGAA
                                            --GGCTACGAATCAATCACCTGATCGACCTGTCTCGCTAC
                                              ||||||||||||||||||  |||||||| | |||||||
       50        60        70        80        90       100       110

     710       720       730       740       750       760       770
CAAACCAGCTTGAACACCCTTGTTAACCTTCTCAGCCAAGGATGGCAGGAAGGTGTAGATCTTGTTAGAGTA
                            ||||||||  |||||||     |||| ||   ||||||||||||||||  |||||
GCTTCCAAAATCAACATCATCGGTTCTTAAAGTTAAC-TTCGATCCGATCGACAGAAATCAGATTCCAGCTGTTCAA
      120       130       140       150       160       170       180

     780       790       800       810       820       830
ACCCAAGGCCTCCTCGACGGAGGTGGTGCTCAAGGTG-AGTTCTCG--------ACGTTGTTAGACAACTTTTG
                  |||| |||  |||    |||| |||||||        |||| ||||||||||||||
TCTGGAATCTTCCAAAATGGAAGTTATCCTGAAGAGTGCTATCGTATACAAACTCATGTACGAAAACTTCTC
      190       200       210       220       230       240       250

     840       850       860       870       880       890       900
AGACTCCAAGTAGTAGTAGGAGTTCAAGTACTCGACGTACTTGGTGATGTCGTGCTGGTAGAAGAGATCTCCCTC
                                           |||||||||||||||||||||||||||| |
CACCTCCTTCTGTCGATCCGTATCCGAAATACTTCAACTCCAT--CTCTCTGAACAATGAATACACCATCATC
      260       270       280       290       300       310       320

     910       920       930       940       950       960       970       980
ACCTGGCAAGTCAATGGCTCCATGTTGACGTTGGCAACAGTGGGTCACGAGTCTGGGTTGATTGGGAC
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AACTGCATGGAAAACAATTCTCGGTTGGAAAGTATCTCTGGAAAGTACACGGTGAAATCATCTGGACTCTGCAGGAC
      330       340       350       360       370       380       390       400

     990      1000      1010      1020      1030      1040
---CTGACGGTCCAGGATGGGACTCG--TCCAAAGAGAACTTGTCCGGAGTAGTTTGAAGGTTGGTCTCGTCG
   |||||||||||||||||||||| ||  |||| |||||||||||||  ||||| |||||||||||||||||||
ACTCAGGAAATCAAACAGCGTGTTGTATTCAAATAACTCTCAGATGATCAACATCTGACTACATCAATCGC
      410       420       430       440       450       460       470

    1050      1060      1070      1080      1090      1100      1110      1120
GTGATGATCTTGTTCTCGGAAGATCCTCCTGGGATGGAGATGGAGTCCTTGTCGGCAACGTATGGCAAGCAGTCGTTGTTC
     ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
TGGATCTTCGTTGTACCATCACCCAACCAATCGTCTGAAGAATAACTCCAAAATCTACCATCACCAACGGCCGTCGTGATCGAC
      480       490       500       510       520       530       540

    1130      1140      1150
TTGACCTTGAT-GCAGTGGAGTCGTCACGGGAGTTGGCCAT              x
     ||||||    |||||||||||||||||||||| |||||
CAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACCATCAATGTTCAAACTGGA
      550       560       570       580       590       600
```

```
2. US-09-910-186A-25' (1-1161)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

   The list of best scores is:
```

```
                           PARAMETERS

Similarity matrix   Unitary     K-tuple              1
Mismatch penalty    1           Joining penalty      30
Gap penalty         5.00        Window size          500
Gap size penalty    0.33
Cutoff score        1
Randomization group 0

                      SEARCH STATISTICS

Scores:       Mean     Median    Standard Deviation
              41       33        8.08

Times:        CPU                Total Elapsed
              00:00:00.00        00:00:00.00

Number of residues:        4027
Number of sequences searched:  3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
100-
    -
    -
 50-
    -
N   -
U M -
B   -
E B -
R R -
    -
 O  -
 F  -
 10-
    -
S   -
 5-
E   -
Q   -
U   -                                                    *
E   -
N   -
C   -
E   -                            *
S   -                *
 0-------|-----|-----|-----|-----|-----|-----|-----|-----|
SCORE 0  |5    10    15    20    26    31    36    41    46
STDEV -4  -3        -2    -1          0
```

Initial Score   =   46   Optimized Score   =   206   Significance = 0.62
Residue Identity =   39%   Matches   =   336   Mismatches   =   236
Gaps   =   26   Conservative Substitutions

```
         560       570       580       590       600       610       620       630
ACCCTCAGGGCGGAGTTACCGATGTTCAAGGCTGACGATGTAGGGATGGGAGGACGTCGGAGAT
            ||||||||   |||   | | ||||||| ||||| |  | |||
          CTCGAGCCATGCGTCGTCTGCTGTCT---ACCTTCACTGAATACATCAAGAA
            x        10        20        30        40

         640       650       660       670       680       690       700
CTTGTCCAGGGTGTCCTTCTTCATGATGGTGGTGAGTCCTCGACGACCTCGTTGGCCCAGTTCAGGAA
  |  ||  ||| |||| || ||  |  ||| |  ||   ||
CATCATCAATACCTCCAATCCTGAACCTG-----CGCTACGACCGTCTCGATCACCTGACCTGTCTCGCTAC
  50        60        70        80        90       100       110

         710       720       730       740       750       760       770
CAAACCAGCTTGAACACCCTTGTTAACCTTCTCAGCCAAGGATGGCAGGAAGGTGTAGATCTTGTTAGAGTA
   |||    | ||||  |||      ||||| |    |   ||| |
GCTTCCAAAATCAACATCGGTTCTAAAGTTAAC-TTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAA
   120       130       140       150       160       170       180

         780       790       800       810       820       830
ACCCAAGGCCTCCTCGACGGAGTGGTGTCAAGGTG-ATGTCTCG-------ACGTTGTTAGACAACTTTTG
  ||||        |        ||||||| | || |||| ||
TCTGGAATCTTCCAAAATCGAAGTTATCCTGGAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTC
  190       200       210       220       230       240       250

         840       850       860       870       880       890       900
AGACTCCAAGTAGTAGGAGTTCAAGTAGTCGACGTACTTGGTTGATGTCGTCGTAGAAGACGATCTCCTC
  ||||         |  ||| |             |||| |
CACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCAT--CTCTCTGAACAATGAATACACCATCATC
  260       270       280       290       300       310       320

         910       920       930       940       950       960       970       980
ACCTTGGCCAAGTTCAATGGCTCCATGTGACGTTTGCAACAGTGGTTCGACGATCTCTGGGTTGATTGGAC
  ||||||   |  ||||||   ||||  ||||  | ||||  ||||||||
AACTGCATGGAAAACAATTCTGATTCTGGTTGGAAAGTATCTGGAACTACGGTGAAATCATCTGGACTCTGGAGGAC
  330       340       350       360       370       380       390       400

         990       1000      1010      1020      1030      1040
AGACTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCAT--CTCTCTGAACAATGAATACACCATCATC
  |||||       |    |||   |  |||||
CCATCTCTGACTCTGCTCCAAGCAGTTCGATGGTCTTGATGATCTTCTCTCTCCTGGATGGAGGA
  410       420       430       440       450       460

         1050      1060      1070      1080      1090      1100
ACCTTGGCAAGTTCAATGGCTCCACATGTTGACGTTTGGCAACAGTGGTCCGACGATGTTGACTTGGAC
  ||||       |    ||      ||      |||   ||||
CGAACTTACAACACCATCCAGATCAAGAATACGACGAACAGCCGACTACTCTTGCCAGCTGCTGTTCAA
  470       480       490       500       510       520       530

         1110      1120
GTTGGATCTTGTTCTCGAAGATCTCCTGGAGAGTCCTTGGACAGTCTTGTCAGTGGATTGGAC
  |||||          |       |       |   ||
GTAGAAGGTGAAGAAGACACCCAGGCTGGGATGTGAACTCTGGGAAACCCTCCAGCTGGAAACCCTCGGAAC
  540       550       560       570       580       590       600

AACTCGCAATACAAACAGCGTGTTGATTCAAAATCTCTCAGATGATCAACATCTCGACTACGATCAATCGC
  |||||||       |       |  |||||
G--AAAGATGAAGAATCTACTGACGAAATCGGTCGATCGGTATCGGAAGATCGGTATCGTA
  610       620       630       640       650       660       670

         1070      1080      1090      1100      1110      1120
GTGATGATCGTTGTCTCGAAGATCTCCTGGAGATGGGAGGAGTCCTTCTTCTGGACAGTCTTGTTC
  |||||||||     |     |||||||   |||
GGTGGCGAAGGCCCTGGTTGAAGT---TACCTCTCAGGCGGAGTTACGAGTTCCAGGCGGAGTTACCGATGTA
  680       690       700       710       720

```

3. US-09-910-186A-25' (1-1161)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score   =   32   Optimized Score   =   246   Significance = -1.11
Residue Identity =   40%   Matches   =   384   Mismatches   =   292
Gaps   =   0   Conservative Substitutions = 51

```
         x         10        20        30        40        50
TTAGTCAACCTCACCAACCAGGATGAGTGATGGGGAGTCCGATCAGGTTGATC
  |||| |      || |    | ||||| ||   |  ||   |
ATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAATATCCAGTCTTACTCCGGAATACCTG
  640       650       660       670       680       690       700
```

```
> O <
O|O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-26.res made by bobryen on Thu 7 Nov 102 14:36:40-PST.

Query sequence being compared:US-09-910-186A-26 (1-386)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

Results of the initial comparison of US-09-910-186A-26 (1-386) with:
       File : US08123975A.pep
```

```
100-
    -
    -
 N  -
 U 50-
 M  -
 B  -
 E  -
 R  -
    -
 O  -
 F 10-
    -
    -
 S  -
 E  5-
 Q  -
 U  -
 E  -
 N  -
 C  -
 E  -                                                           *
 S  0-|---|---|---|---|---|---|---|---|---|---|
SCORE 0   22  44  67  89  111 133 156 178 200
STDEV     0   0            1   1

              PARAMETERS

Similarity matrix     PAM-150     K-tuple              1
Threshold level of sim.  16%      Joining penalty     20
Mismatch penalty         1        Window size        386
Gap penalty           5.00
Gap size penalty      0.05
Cutoff score          1
Randomization group   0

              SEARCH STATISTICS

Scores:        Mean     Median    Standard Deviation
                78        17            105.38

Times:    CPU                  Total Elapsed
      00:00:00.00              00:00:00.00

Number of residues:              1704
Number of sequences searched:       3
Number of scores above cutoff:      3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                                     Init.  Opt.
Sequence Name    Description                            Length Score Score  Sig. Frame
-------------    -----------                            ------ ----- -----  ---- -----
                 **** 1 standard deviation above mean ****  850   200   262   1.16   0
1. US-08-123-975A-2 Sequence 2, Application              262   200   262   1.16   0
                 *** 0 standard deviation from mean ***  415    19    19  -0.56   0
2. US-08-123-975A-3 Sequence 3, Application              170    19    16  -0.56   0
3. US-08-123-975A-5 Sequence 5, Application              439    16   101  -0.59   0
```

```
1. US-09-910-186A-26 (1-386)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score      =  200    Optimized Score   =  262    Significance =  1.16
Residue Identity   =  37%    Matches           =  143    Mismatches   =  208
Gaps               =   2     Conservative Substitutions =    29

              X  10        20        30        40        50        60        70
MANSRDDSTCIKVKNNRLPYVADKDSISQEIFENKIITDETNVQNYSDKFSLDESILDGQVPINPEIVDPLL
         |    | ::||||::|     |        |||  | : ||||
APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENT
    X     10        20        30        40        50        60
          80        90       100       110       120       130       140
PNVNMEPLNLPGEIVFDDITKYVDYLNSYYLESQKLSNNVENITLTTSVEEALGYSNKIYTFLP-SLAE
   :|||||| | || ||||||||||||||||||||||||||||||:|||| | |:| ||||  ||
ESLTDFNVDVPVYEKQ-PAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIK
70        80        90       100       110       120       130
         150       160       170       180       190       200       210
KVNKGVQAGLFLNWANEVVEDTTNIMKKDTLDKISDVSVIIPYIGPALNIGNSALRGNFNQAFATAGVAFL
         |||     |       |  ||  :  | |  |:  :| | | | |    ||  |  |
TANKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLTVPYIGLALNVGNETAKGNFENAFFIAGASIL
140       150       160       170       180       190       200       210
         220       230       240       250       260       270       280
LEGFPEFTIPALGVFTYSSIQEREKIIKTIENCLEQRVRWKDSYQWMVSNWLSRITTQFNHINYQMYDSL
||   :  |  |:| || ||  || ||:| :  |    |  :|  :  |  |:|  |  :|   |:  :
LEFIPELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKAL
220       230       240       250       260       270       280
         290       300       310       320       330       340       350
SYQADAIKAKIDLEYKKYSGSDKENIKSQVENLKNSLDVKISEAMNINKFIRECSVTYLFKNMLPKVIDEL
    |  || |       |    :|:|  : ||  | |||  ||  |||| ||||  : |  |||||
NYQAQALEIIKYRNYIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEKL
290       300       310       320       330       340       350
         360       370       380
NKFDLRTKTELINLIDSHNIILVGEVD       X
|| ||  | || || |  ::|:|
LFPDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSI
360       370       380       390       400
```

```
2. US-09-910-186A-26 (1-386)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score      =   19    Optimized Score   =   19    Significance = -0.56
Residue Identity   =   11%    Matches           =   44    Mismatches   =  314
Gaps               =    9     Conservative Substitutions =    28

              X     10        20        30        40        50        60        70
          MANSRDDSTCIKVKNNRLPYVADKDSISQEIFENKIITDETNVQNYSDKFSLDESIL
              X  10        20        30        40        50        60        70
RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYF
          60        70        80        90       100       110       120
DGQVPINPEIVDPLLPNVNMEPLNLPGEIVFDDITKYVDYLNSYYLESQKLSNNVENITLTTSVEEALG
    :  :  :  | | :   | :|| |   ||  | | ::|  | |  |  :||::|   |
NSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLN
          80        90       100       110       120       130       140
```

```
130                140        150        160        170        180        190
YSN-----KIYTFLPSLAEKVNKGVQAGLFLNWANEVVEDFTNIMKKDTLDKISDVSVIIPYIGPALNIGN
NSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGIL
        150        160        170        180        190        200        210

200        210        220        230        240        250        260
SALRGNFNQAFATAGVAFLLEGFPEFTIPALGVTFYSSIQEREKIIKT---IENCLEQRVKRWKDSYQWMV
KDFWGDYLQYDKPYYMLNLYDPNKYDVNNVGIRGVMYLKGPRGSVMTNIYLNSSLYRGTKFIIKKYASGN
220        230        240        250        260        270        280

270        280        290        300        310        320        330
SNWLSRITTQFNHINYQMYDSLSYQADAIKAKIDLEYKKYSGSDKENIKSQVE-NLKNSLDVKISEAMNNIN
KDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKMNLQD
290        300        310        320        330        340        350        360

340        350        360        370        380            X
KFIRECSVTYLFKNMLPKVIDELNKFDLRIKTELINLIDSHNIILVGEVD
NNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL
370        380        390        400        410
```

3. US-09-910-186A-26 (1-386)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

```
Initial Score   =   16    Optimized Score   =   101   Significance =  -0.59
Residue Identity =  8%    Matches           =   88    Mismatches   =   204
Gaps            =         Conservative Substitutions =  6              = 17
```

```
           X       10        20        30             40
           MANSRDDSTCIKVKNNRLPYVADKDSISQEIFENKIITD-----ETNVQNY
SNTDIKDIREVIANGEIIFKLDGDIDRTQFTWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYN
180        190 X     200        210        220        230        240

50        60        70        80        90        100        110
SDKFSLDESILDGQVPINPEIVDPLLPNVMEPLNLPGEEIVFYDDITKYVDYLNSYYYLESQKLSNNVENI
KEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYI
250        260        270        280        290        300        310

120        130        140        150        160        170        180        190
TLITSVEEALGYSNKIYTFLPSLAEKVNKGVQAGLFLNWANEVVEDFTNIMKKDTLDKISDVSVIIPYIGP
YLDFFNLNQEWRYYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIG
320        330        340        350        360        370        380

200        210        220        230        240  X     250        260
ALNIGNSALRGNFNQAFATAGVAFLLEGFPEFTIPALGVFTFYSSIQEREKIIKTIENCLEQRVKRWKDSYQ
IHRFYESGIVFEEYKDYFCISKKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE                X
390        400        410        420        430
```

```
> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-27.res made by bobryen on Thu 7 Nov 102 14:49:17-PST.

Query sequence being compared:US-09-910-186A-27 (1-1149)
Number of sequences searched:          3
Number of scores above cutoff:         3

Results of the initial comparison of US-09-910-186A-27 (1-1149) with:
    File :US08123975A.seq
```

```
Sequence Name      Description                              Length  Init. Opt.
                                                                    Score  Score  Sig.  Frame
-----------------------------------------------------------------------------------------------
                   **** 1 standard deviation above mean ****
1. US-08-123-975A-6 Sequence 6, Application U  1351           98    463    1.15    0
                   **** 0 standard deviation from mean ****
2. US-08-123-975A-4 Sequence 4, Application U  1338           86    408   -0.58    0
3. US-08-123-975A-1 Sequence 1, Application U  1338           86    408   -0.58    0
```

```
1. US-09-910-186A-27 (1-1149)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score      =    98    Optimized Score        =   463    Significance =   1.15
Residue Identity   =   43%    Matches                =   561    Mismatches   =   576
                              Conservative Substitutions =  144    Gaps         =     0
```

```
               X          10        20        30        40        50
               ATGTCCATCTGCATCGAGATCAACAACGGTGAGCTGTTCTTCGTGGCTTCCG
               |||  ||| ||    ||  | |||||  |  || |  |||| |||
ACAATTCCGAAATCCTGAACAATCATCCTGAACCTGCGTTACAAAGACAACAATCTGATCGATCTGTCTG
20        30     X 40        50        60        70        80

                   60        70        80        90       100       110
               AGAACAGTTACAACGATGACAACATCACACTCCTAAGGAGAGATTGACGA--------CACCGTCACTTCTA
               | || |  || | || ||| || | | ||  ||||   |  ||| ||        || | ||| |||
GTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAAGTGACAAGAACCAGTTGAAACTGACCTCTT
90       100       110       120       130       140       150       160

                  120       130       140       150       160       170       180
               ACAACAACTACGAAAACGACCTGGACCAG---GTCATCCTAAACTTCAACTCCG-AGTCCGCCCCTGGTCTG
               | |||| | |    || ||| |||| ||   ||  |||  | |||||||||  | || ||  ||| ||
CCGCTAACTCTAAGGATCCGTATCCGTGTTACTCAGAATCAGAACAATCATCTCCGTATTCCTGGACTTCCTG
170       180       190       200       210       220       230

                  190       200       210       220       230       240       250
               --TCCGACGGAAGCTGAACCTGACCATCCAGAACGACGCCTTACATCCCAAAGTACGACTCCAACGGTACAT
                 ||| ||  | |   || ||||| | ||||   | |||| | || ||  |||    |||| ||  |||
TTTCCTTCTGGATCCGTATCCCGAAATACAAGAACGACGGT---ATCCAGAATTACATTACACCACAA-TGAATAC
240       250       260       270       280       290       300

                  260       270       280       290       300       310       320
               CCGATATCGAGCAGCAGCATGACG-TTAACGAGCTT--AACGTCTTCTTCTACTTAGACGCCTCGGAAGGTGCCC
               ||   ||  ||| ||  ||  ||||  || |||||    ||  |||| | |  | |||  | |  || |||
ACCATCATCAACTGCATGAAGGAATAACTCTGGTTGGAAGATCCCATCCGCGGTAACCGTATCATCTGGACT
310       320       330       340       350       360       370

                  330       340       350       360       370       380
               GAGGGTGAGAACAACG------TCAATCTCACCTCTCAATTGACACAGCCTTGTTGGAGCAGCCTA--AG
               |  ||| ||  | ||        || |||| |   | | |||  | ||||| || ||  || ||
CTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTCGAATACAACAATCCGTGAAGACAATCTCTGAATAC
380       390       400       410       420       430       440

                  390       400       410       420       430       440       450
               ATCTACACCTTCTTCTCCTCCGAGTTCATCAACAACGTCAACAAGCCTGTGCAGGCGCCATTGTTCGTAAGC
               | |  || || | |||| ||  ||  || | |||  |||  ||| |  | ||    |   | |||| |||
ATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGC--TAAAATCTACATCAACGGTAAAC
450       460       470       480       490       500       510

                  460       470       480       490       500       510       520
               TGGATTC--AGCAGGTGTTAGTAGACTTCACT---ACTGAGGTAACCAGAAGTCCACTGTTGACAAGATCG
               ||   ||   || ||||| ||| |||  |||     ||| | | |  ||| ||  || |||  |||| ||
TGGAATCTAATAACCGACATCAAAGACATCCGTGAAGTTATCGCTGAAGTTGAAATCATCTTCAAACTGGACG
520       530       540       550       560       570       580

                  530       540       550       560
               CTGACATC-------------------------TCCATCGTCGTCCCATCATCGGTCTCGGCTCTGAACA
               |||||||                          ||   | | |  || | ||||  ||| || | ||
GTGACATCGATCGTACCCAGTTCATCTGGATGAAGAAATACTTCGTCCATCTCAACACCGAACGTGTCCAGTCCA
590       600       610       620       630       640       650

                  570       580       590       600       610       620       630
               TCGGCAACGAGGCACAGAGGGC-------AACTTCAAGGAGATGCCCTTGAGTTGTTGGGTGCCGGTATTTGT
```

```
                        SCORE  STDEV
100-
    -          *
  N -
  U 50-
  M -
  B -
  E -
  R -
    -
  O -
  F 10-
    -
  S -
  E 5-
  Q -
  U -
  E -
  N -
  C -
  E -
  S -
    0------------------------------------------------------------------------------
       |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
       -9  -8  -7  -6  -5  -4  -3  -2  -1   0
  SCORE 0   11  22  33  44  54  65  76  87  98
  STDEV                                         *
```

```
                PARAMETERS
Similarity matrix    Unitary
Mismatch penalty     1             K-tuple           4
Gap penalty          5.00          Joining penalty   30
Gap size penalty     0.33          Window size       500
Cutoff score         0
Randomization group  0

                SEARCH STATISTICS
              Mean      Median     Standard Deviation
Scores:         90        87              6.93

              CPU                  Total Elapsed
Times:      00:00:00.00           00:00:00.00

Number of residues:          4027
Number of sequences searched:   3
Number of scores above cutoff:  3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

AAACGACCTGGACGTCATCCTAAACTTCAACTTCACTTCCGAGTCCGCCCCTGGTCTGTCCGACGAGAAGCTGAA
|||| |||||||| |||||||| ||||||||||||||||||||||||| |||
ACATCATCAATACC--TCCATCCTGAACCTGCCGCTACGAAT--CCAATCACCTGATCGACCTGTCTCGCGTA
50   60   70   80   90   100   110

CCTGACCATCCAGAACGACGCTTACATCCCCAAAGTACGACTCCGATCGACAGAGAACAGCAGCATGA
|||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||||||||||||||||
CGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGACAAGGAATCAGATCCAGCTGTTCAA
120   130   140   150   160   170   180

CGTTAACGAGCTTAACGTCTTCTTCTACGTTACTTAGACGCTTCAGAAGGTGCCCGAGGGTGAGAAC--AACGTCAA
||||||||| ||||||||||||||||| ||| |||||||||||||||||||||||||| |||
CGGTGAATCTTCAAAATCGAAGTATCCTGAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTC
190   200   210   220   230   240   250

TCTCACCCTTCAATTGACACAGCCTGTTGGAGCAGCCTAAGATCCATCACCTTCTTCCTCCGAGTTCAT
|| ||||||| |||||||||||||||||||||||||||||||||||| |||||||||||||||||||
CACCTTCCTTCTGCGATCCGTATCCCGAAATACTTCAACTCCATCCTCTGAACAATGAATACCACCATCATCAA
260   270   280   290   300   310   320   330

CAACAACGTCAACAGCCTGTCGAGCGCCGCATTGTT--CGTAAGCTGATTCAGCAGGTGTGTAGTAGACTTC
||||| |||||||||| |||||||||||| ||| |||||||||||||||||||||||
CTGCATGGAAAACAATTCTGGTTCGGAAGAGTATCTCTGAAATCATCGTGAAATCTGAACTACGGTGAG----
340   350   360   370   380   390

ACTACTGAGGCTAACCAGAAGTCCATCTGTGACAAGATCGCTGACATCTCCATCATCGGT
||||||||||||||| |||||||||||||||||||||||||||||||||||
GACACTCAGGGAATCAACAGCAGCTGGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACTACCAT
400   410   420   430   440   450   460   470

--AACTTCAAGGATGCCCTTGAG-TT
||||||||||||||||||| || ||
--CTCGGCTC----TGAACATGGAGTTACCATCACCAACAATCGCTGAATAACTCCAAAATCTTCAACTACATC
480   490   500   510   520   530   540

GTTGGGTGCCGGTGATTTGTTGGAGTTCGAACCCGAGCTGCTGATCCTACCATCCTGGTCTTCACGATCAA
|| ||||||||| ||||| |||||||||||||||| ||||||||| |||||||||||||||
GACCAGAAACGATCTCCAATCTGGGTAACATCACCAGCGTTCTAA---TAACATCATGTTCAAACTGGGACGG
550   560   570   580   590   600   610

GTCCTTCCTGGGTCCTCCGACAACAAGAAGTCATTAAGGCCATCACAGAAGTCATTAGCCAGCGACGTGA
|||| ||||||||||||||||||| |||||||||| ||||||||||| |||||||||||||||
TTGTCGTGACACTCACCGTACACTACACCAACAAGTTCAATCTGTTCGACAAAAAGACTGAACGAAAAGA
620   630   640   650   660   670   680

---CGAGAAGTGAAGGAAGTGTATTCCTTCATCGTCTGCAACTGATGACCAGATCAACAACACC--CAGTT
||||||||||||| ||||||||||||| | |||||||| ||||||
AATCAAAGAACCTGTACGACAACCAGTCCAATTCTGTGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTA
690   700   710   720   730   740   750

CAACAAGCGAAAGGAGCAGATGTACC---AGGCTCTGCAGAATCCGAACAACCAGTCAACGCCATCAA---GACCATCAT
|||| ||||||||||| |||||||||||||| ||| ||||||||||| |||||||
CGACAAACCTGACTACTACGTTACGATCCGAATCTGTACGACAATAACGTTGAGCATGTTAGGTAGTATCCG
760   770   780   790   800   810   820

CGAGTCCAAGTACAACTCCTACACCTACACCCTGGAG----GAGAAGAACGAGCTTACCAACAAGTACGATATCAAG
|| | ||||||||||||||||| ||||| | ||||||||||||||||||||||| ||
CGGTTACATGTAC--CTGAAAGGTCCCGTGGTTCGTGTTCTGTTATGACTACTACCCTTCAACTTCCCCTG
830   840   850   860   870   880   890

CAGATCGAGGAACGAGCTGAACCAGGAGTCTCCATCCGGGCCATGGAACAACATCGACA-GGTTCCTGACCGAGTC
960   970   980   990   1000   1010   1020

```
3.  US-09-910-186A-27 (1-1149)
    US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score        =  86      Optimized Score          =  408     Significance    = -0.58
Residue Identity     =  43%     Matches                  =  478     Mismatches      =  571
Gaps                 =          Conservative Substitutions =  62                      0
```

```
> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-27-inv.res made by bobryen on Thu 7 Nov 102 14:49:34-PST.

Query sequence being compared:US-09-910-186A-27' (1-1149)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

Results of the initial comparison of US-09-910-186A-27' (1-1149) with:
File :US08123975A.seq
                                                         complement
```

```
100-
    -
    -
N   -
U   -    50-
M   -
B   -
E   -
R   -
    -
O   -
F   10-
    -
S   -
E    5-
Q   -
U   -
E   -
N   -                                                          *
C   -
E   -                                          *
S   - ------------------------------------------------------------
    0-  |   |   |   |   |   |   |   |   |   |   |   |   |   |   |40
SCORE 0  4   9  13  18  22  27  31  36  -1
STDEV         -9  -8  -7  -5  -4  -2  -1   1
```

```
                    PARAMETERS

Similarity matrix    Unitary        K-tuple              4
Mismatch penalty     1              Joining penalty      30
Gap penalty          5.00           Window size          500
Gap size penalty     0.33
Cutoff score         1
Randomization group  0

                    SEARCH STATISTICS

Scores:       Mean     Median        Standard Deviation
              38       38            1.73

Times:        CPU                    Total Elapsed
              00:00:00.00            00:00:00.00

Number of residues:            4027
Number of sequences searched:     3
Number of scores above cutoff:    3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                              Init.  Opt.
Sequence Name   Description                       Length Score Score  Sig. Frame
-------------   -----------                       ------ ----- -----  ---- -----
                **** 1 standard deviation above mean ****
                **** 0 standard deviation from mean ****
 1. US-08-123-975A-6 Sequence 6, Application U 1151   40   359  1.15    0
 2. US-08-123-975A-4 Sequence 4, Application U 1338   37   400 -0.58    0
 3. US-08-123-975A-1 Sequence 1, Application U 1338   37   400 -0.58    0

 1. US-09-910-186A-27' (1-1149)
    US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score      =   40   Optimized Score     =  359   Significance  =  1.15
Residue Identity   =  40%   Matches             =  416   Mismatches    =  569
Gaps               =   54   Conservative Substitutions  =    0
```

```
     120       130       140       150       160       170       180       190
GAGGACTCGGTCAGGAACCTCGCGATGTTGTTCATGCCGATGGAGACCTTCTCGGTTCAGCTCGTTCGTTCTCGATC
   |  ||  ||  |  | ||    | |   |||| ||  | ||      | |  |  | || ||| |  | || |
                  ATGGCTTTCAACAAATACAATCCTGAACATCCTGAACAATATCATCCTGAACC
                    X         10        20        30        40        50

     200       210       220       230       240       250       260
TGCTTGATATCGTACTTGTTGGTAAGCTCGTTCTCTCCCTCCACGGTGTAGGAGTTGTACTTGGACTTCGATG
|||||||| | | | |  |   ||  | ||  |   | ||||    |   | |  || ||  ||| | | | |||
TGCGTTA---CAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTG
       60        70        80        90       100       110       120

     270       280       290       300       310       320       330
ATGGTCTTGATGGCGGTTGACCTGGTTCTGCAGAGCCTGGTACATCGTCCTTTCGCTTGTTGTGAACTGGGTG
|| |  || |   |  |  | | |  |   |    | ||    | |  |  |||  ||  | | | ||||  |
TTGAACTGAATGACAAGAACCAGTTCAAACTGA-CCTCTTCCGCTAACTCTAAGATCCTGGTGTTACTCAGAAT
      130       140       150       160       170       180       190

     340       350       360       370       380       390       400
TTGATCTTGGTCATCCAGTTCGAGACGATGGAGGAATAGACTTCTCGTTTCCTTCCACTTCTCGTCACGCTCCTTCAGG
||| | ||  |  |    ||  | |   |  | ||   | | |   |  ||  |||  || | |   ||  | | | |
CAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTCCTGGATCCGATCCGTATCCCGAAAATACAAG
      200       210       220       230       240       250       260

     410       420       430       440       450       460       470
GCGTTGTTGATGGCCTTAATGACCTTGTTCTTGTTGTCGGAGGAACCCAGGAAGGACTTGATCGTGAAGACC
  | ||  | ||   | |  |  |  |    || |      |  ||| ||| | |  | |  ||||| |  |||
--AACGACGGTATCCAGAATTACATCCACAAT------GAATACACCATCAACTGCATCGCATGCAATGAATAAC
      270       280       290       300       310       320

     480       490       500       510       520       530       540
AGGATGGTAGGGATGCAGCTCGGGTTCGAACTCCAACAAAATACCGGCACCCAACAAC-TCAAGGGCATC
||||  | |  | | ||| |  |||    |   ||| | |||  | ||| || |||| | ||||| |||
TCTGGTTGGAAGATCTCCATCCGCGTAACCGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAA
     330       340       350       360       370       380       390

     550       560       570       580       590       600       610       620
CTTGAAGTTGCCCTTCGTGCCTCGTTGCCGATGTTCAGAGCCAGACCGATGTATGGACGACCGATGGCGACGATGGAGAT
||| | ||| |   || |  | ||  ||     |  || | |  |   | |     |||  |   | ||| | | | ||||
TCTGTATTCTTCGAATACAACATCCGTGAAGACATCTCTGAAGACAATCATCGCTGGTTCTTCGTT---ACC
      400       410       420       430       440       450       460

     630       640       650       660       670       680       690
GTCAGCGATCTTGTCAACAGTG--GACTTCTGGTTAGCCTCAGTAGTGAAGTCTACTAACACCTGCTGAATC
|| |  |||| |||  |  | ||  ||||  |  | |  |  |   | ||| ||   | |  |    ||  ||
ATCACCAATAACCTGAACAATGCTAAAATCTTACACCGTAAAATCTAACTGGAATCTAATACCGAACATCAAAGAC
      470       480       490       500       510       520       530       540

     700       710       720       730       740       750
CAGCTTACGAACAATGCGGCCTGCACAGGCTTGTT------GACGTTGTTGATGAAC--TCCGGAGGAGAAG
|| ||  |   |  ||  |   || | ||| ||     ||  | ||| || |     | |  || || |||
ATCCGTGAAGTTATCCGTAACGGTGAAATCATCTTCAAACTGGACGTTGACCGTGACATGCGTACCCAGTTCATC
     550       560       570       580       590       600       610

     760       770       780       790       800       810       820
AAGGTGTAGATCTTAGGCTGCTCCAACAAGG--CTGTGTCAATTGAAGAGGTGAGAATTG--ACGTTGTTCTC
```

2. US-09-910-186A-27' (1-1149)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score   = 37   Optimized Score   = 400   Significance = -0.58
Residue Identity   = 40%   Matches   = 464   Mismatches   = 610
Gaps   =   Conservative Substitutions = 61   Gaps   = 0

3. US-09-910-186A-27' (1-1149)

US-08-123-975A-1 Sequence 1, Application US/08123975A

```
Initial Score   =   37   Optimized Score  =   400   Significance  =  -0.58
Residue Identity =  40%  Matches          =   464   Mismatches    =   610
Gaps            =         Conservative Substitutions =   61                 0
```

```
            40         50         60         70         80         90        100
AGGTACTCTTGACAATCTCGTCGTACTCCGCAGCTTGTTGATCTTGACCTGGTTCATGAGCTTCATCAGG
                           ||||         ||       ||||||||||  ||||||||||||
             CTCGAGCCATGGCTCGT-----CTGCTGTCTACCTTCACTGAATACATCAAG
                           x              10              20        30        40
```

```
    110        120        130        140        150        160        170        180
TAGGAGATGGAGGACTCGGTCAGGAACCTGCGATGTGTTCGATGTTCTGGATGGGCTGGAGACCTTCTGTTCAGCTCG
      |||      |||   ||||||  ||||||                      |||||||||  ||||| |||
AACACATCATCAATACCTCCAACCTTGCGCTGACCTGCGATCCTGCTACGACCTGTCGCCGGCT
    50              60              70              80              90       110
```

```
        190        200        210        220        230        240
TTCTCGATCTGCTACGTACTTGTTGGTAAGCTCGTTCTTCTCCCCCAG------GGTGTAGGAGTTGT
            |||       |||||||||||       ||| |||||  |||||||||||||
        TCCAAAAATC-----AACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCA
          120              130              140       150        170        180
```

```
    250                260        270        280        290        300        310
ACTTGACTC------GATGATGGTCGTTGATGGGCGGTTCTGCAGAGCCTGGTAC---ATCTGCT
    |||||      ||||       ||||  |||||||      |||||||  ||  |||
ATCTGGAATCTTCCAAAATGAAGTTATCCTGAAGAATGCTATCGTATCAACTCTATGTACGAAAACTTCT
    190              200              210        230        240        250
```

```
            320        330        340        350        360        370        380
CCTTCGCTTGGTTGACTCGGGTGTTGATCTTGGTCATCCAGTTCGAGACGATGAAGGAATAGACTTCCTTCC
        |||||                   ||||||     |||||||        |||
CCACCTCCTTCGGATCCGTATCCGAAATACTTCAACTCATCTCTGAACAATGAATACACCATCATCA
    260              270        290        300        310        320        330
```

```
    390        400        410        420        430        440        450
ACTTCTCGTCACGC---TCCTTCAGGCGGTTGTTGATGGCCTTAATGACCTTGTTCTTCGTTGTCGGAGGA-A
|||||         |||||||||  |||||||          ||||||         ||||       |||
ACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCGAAAGTTCTGAAACTCTGAAATCATCTGAACTACGCAGGACA
    340              350        360        370        380        390        400
```

```
            460        470        480        490        500        510
CCCAGGAA---GGACTTGATCGTGAAGACCAGGATGGTAGG--GATCAGCAGCTCGGGTTCGGAACTCCAACA
|||||||      ||||||           ||||||||          |||||    |||
CTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTGAATGATGATCAGATGAACAAACATCTGAACTACGCT
    410              420        430        440        450        460        470
```

```
    520        530        540        550        560        570        580        590
AAATACCGGCACCCCAACAACTCAAGGGCATCCTGAAGTTGCCCTTCGTGTCCCGATGTTCCGATGTTCAGAG
||||||||                                |||||        |||||||       |||
GGATCTTCGTTACCATCACCAACAACATCAGTGATCCTGAATAACTCTGAAATCTACAACATGGTCGACC
    480              490        500        510        520        530        540
```

```
            600        610        620        630        640        650        660
CCAGACCGATGATGGAGGGAGGAGAGCGATGGAGAGTGCAGCAGCGATCGTTCCAACAGTCGTCGTTAGCCTCAG
||||||||                                       ||||||||||       |||
CTCAGGAAATCAAACAGCGTGTTGTATTCAAATCTCTTAATAACTCTGGTACCACTGGACGGTTG
    550              560        570        580        590        600        610
```

```
    670        680        690        700        710        720        730
AGAAACCGATCT-----CCAATCTGGGTACCATCCACGCATCTAATAACTTCAATCTGTTGACAAACTGGACGGTTGT
|||||||                 |||||||      ||||||         ||||||         ||
TCGTGAACTACTAACACCGGTCACTGTCAACATTCCTGGTATCCGGTATCCTGGTATCCTGGGGGTGACTACCTGCAGTA
    620              630        640        650        660        670        680
```

```
            740        750        760        770        780        790        800
TGATGAACTCGGAGGAGAAGAGCGTGAACGCAACCAG---TCCAATTCTGGTATCCGGATCTTCGTGAAGAGGGTG
            ||||||||            ||||         ||||||||        ||||
CAAAGACCT-GTACGCAG-GTACGCAACAACATCCTGGGGGTGACTACCTGCAGTA
    690              700        710        720        730        740        750
```

```
    810        820        830        840        850        860
                860
```

AGATTGACGTGTGTT--CTCACCCTCGGGCACCTTCTGAGCGTCAAGTAGAAG------AAGACGTTAAGCT
                                                              | ||| | |||
CGACAAACCGTACTACAGTCGTGAATCGCTGAAATCGATCCGGAACAAAATACGTTGACGTCAACAATGTAGGTATCCG
    760   770   780   790   800   810   820

```
870        880        890        900        910        920        930
CGTTAACGTCATGTCGTCGATATCGGATGTTACCGT--TGGAGTCGTACTTTGGGATGTAAGCGTC---GTT
|||||||||             ||||||||||||||  |||||||||         ||||    |||  ||
CGGTTACAGTGTACCTGAAAGTCCGCGCTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTA
    830        840        850        860        870        880        890
```

```
    940        950        960        970        980        990       1000
CTTGGATGGTCAGGTTCAGCTTCCTCGTCGGAC-AGACCAGGGGCGACTCCGAGTTGAAGTTAGGATGACCT
||||||||         ||||||             |||||||||       ||||||||||||||
CCGTGGTACCAAAATTCATCATCAAGAACATACGGCGTCTGTAACAAGGACAATATCGTTCGCAACAATGATCG
    900        910        920        930        940        950        960       970
```

```
    1010       1020       1030       1040       1050       1060       1070
GGTCCAGGTGCGTTTCGTAGTTGTTGTTAAGAACGTCACGGTGTCCAATCTCCTTAGGAGTGTTGATGTTGT
      |||||||         |||||||||||         ||||||||||||       |||||||||
TGTATACGCAATGTGTAGTTGTTAAGACAAGAATACCCGGTAATCTGCTACCATCGCTTCTCAGGCGTGGTGTGAGA
    980        990       1000       1010       1020       1030       1040
```

```
    1080       1090       1100       1110
CATCGTTGTAACTGTCTCGGAAGCCACGAAG----AACAGCTCACCGTTGTTGATCTGGCAGATGGA
|||||||         |||||||||||||         |||||||||||||||||||
AAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTTCTCAGTAGTTGTAATGAAATCCAAGAA
    1050       1060       1070       1080       1090       1100       1110
```

```
x
CAT
CGACCAGGGTATCACTAACAAAT
    1120       1130
```

```
> O <
O| |O   IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-28.res made by bobryen on Thu 7 Nov 102 14:37:06-PST.

Query sequence being compared:US-09-910-186A-28 (1-382)
Number of sequences searched: 3
Number of scores above cutoff: 3

```
100-
    -
 50- -
    -
N   -
U   -
M   -
B   -
E   -
R   -
    -
O   -
F 10-
    -
S   -
E  5-
Q   -
U   -
E   -
N   -
C   -     **
S  0- ----|----|----|----|----|----|----|----|----|----|
SCORE 0   20   40   59   79   99  119  138  158  178
STDEV 0    0    1    1    1    1    1              *
```

PARAMETERS

Similarity matrix	PAM-150	K-tuple	1
Threshold level of sim.	16%	Joining penalty	20
Mismatch penalty	1	Window size	382
Gap penalty	5.00		
Gap size penalty	0.05		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

	Mean	Median	Standard Deviation
Scores:	69	15	93.83

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues: 1704
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
                                                         Length  Init. Opt.
Sequence Name    Description                                     Score Score Sig. Frame
---------------  -------------------------------------------     ----- ----- ----- -----
                 **** 1 standard deviation above mean ****
1. US-08-123-975A-2 Sequence 2, Application U             850   178   270   1.16   0
                 **** 0 standard deviation from mean ****
2. US-08-123-975A-3 Sequence 3, Application U             415    17   175  -0.55   0
3. US-08-123-975A-5 Sequence 5, Application U             439    14   173  -0.59   0
```

1. US-09-910-186A-28 (1-382)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

```
Initial Score     =  178    Optimized Score =  270    Significance  =  1.16
Residue Identity  =  41%    Matches         =  157    Mismatches    =  185
Gaps              =    7    Conservative Substitutions      =         33
```

```
        X        10        20        30        40        50        60        70
   MSICIEINNGELFFVASENSYNDDNINTPKEIDDTVTSNNYENDLDQVILFNSESAPLSDEKLNLTIQ
   |||:| | :|||  |  |  | :  :     |:     :  |   |||   | | :      ||
APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLLISKIELPSENTESLTD
   X        10        20        30        40        50        60        70

            80        90       100       110       120       130       140
NDAYIPKYDSNGTSDIEQHDVNELNVFFYLDAQKVPEGENNVNLTSSIDTALLEQPKIYTFFSSEFINNVNK
 :|:  |        |  ||    |:      :||||||    ||| ||    |  ||:||  :   |  :|  ::|
FNVDVPVYEKQPA--IKKIFDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIKTANK
            80        90       100       110       120       130       140

      150       160       170       180       190       200       210
PVQAALFVSWIQQVLVDFTTEANQKSTVDKIADISIVVPYIGLALNIGNEAQKGNFKDALELLGAGILLEFE
 |:|:   |     :  |||  :|: |||||||||||  ::|||:|:|  |||||:|||:||||||||||||:
VVEAGLFPAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLA-NVGNETAKGNFENAFEIAGASILLEFI
      150       160       170       180       190       200       210

      220       230       240       250       260       270       280
PELLIPTILVFTIKSFLGSSDNKNKVKAINNALKERDEKWKEVYSFIVSNWMTKINTQFNKRKEQMYQALQ
 ||||| :| |  |:   | |||||||| ||||| | ||:||||||||||||||||| |||  |  |||
PELLIPVVGAFLLESYI---DNKNKIIKTIDNALTKRNEKWKSDMYGLIVAQWLSTVNTQFYTIKEGMYKKALN
      220       230       240       250       260       270       280

      290       300       310       320       330       340       350
NQVNAIKTIIESKYNSYTLEEKNELTNKYDIKQIENELNQKVSIAMNNIDRFLTESSISYLMKLINEVKINK
 | |  |:| | | |  :|:|| || ||:   ||| ||||  :||  ||:|   ||   ::|:||| |:| |||
YQAQALEIIKYRYNYISEKEKSNI--NIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEK
      290       300       310       320       330       340       350

360       370       380 X
LREYDENVKTYLLNYIIQHGSIL
 |  ::  |   |||||
LLDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMP
360       370       380 X  390
```

2. US-09-910-186A-28 (1-382)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

```
Initial Score     =   17    Optimized Score =  175    Significance  = -0.55
Residue Identity  =  10%    Matches         =   40    Mismatches    =  320
Gaps              =    6    Conservative Substitutions      =         22
```

```
        X        10        20        30        40        50        60
   MSICIEINNGELFFVASENSYNDDNINTPKEIDDTVTSNNYENDLDQVILFNSESAPLSDEKLN
                :  |  |  |:  :    :      ||  : :        |  :||
RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYF
   X        10        20        30        40        50        60        70

       70        80        90       100       110       120       130
LTIQNDAVIPKYDSNGTSDIEQHDVNELNVFFYLDAQKVPEGENNVNLTSSIDTALLEQPKIYTFFSSEFIN
  :   :                     :          ||     |  :| :   || :   :|    |:
NSISLNEYTIICMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLN
       80        90       100       110       120       130       140
```

```
140          150       160       170       180       190       200       210
NVNKPVQAALFVSWIQQVLVDFTTEANQKSTVDKIADISIVPYIGLALNIGNEAQKGNFKDALELLGAGIL
     |  :::|    |   | | |     -|   |  |||        |||          :|||
NSKIYINGRLIDQKPISNLGNIHASNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGIL
150          160       170       180       190       200       210

   220       230       240       250       260       270       280
LEFEPELLIPTILVFTIKSFLGSSDNKNKVIKAINNA-LKERDEKWKEYYSFIVSNWMTKINTQFNKRKEQM
:|  |---|             :|            |  ||  ||           :|       |
KDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTNIYLNSSLYRGTKFIIKKYASGN
220          230       240       250       260       270       280

   290       300       310       320       330       340
YQALQNQVNAIKTIIESKYNSYTLEEKNELTNKYDIKQI-----ENELNQKVSIAMNNIDRFLTESSISYLM
  :  :     |     |                  |     -       |
KDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKMNLQD
290          300       310       320       330       340       350       360

350          360       370       380 X
KLINEVKINKLREYDENVKTYLLNYIIQHGSIL
|::  |             ||   |
NNGNDIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGER
370          380       390 X      400       410


3. US-09-910-186A-28 (1-382)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =    14   Optimized Score    =   173   Significance = -0.59
Residue Identity =   11%   Matches            =    50   Mismatches   =  296
Gaps             =    51   Conservative Substitutions =  29

X           10        20        30        40        50        60
MSICIEINGELFFVASENSYNDDNINTPKEIDDTVTSNNYENDLDQVILNFNSESAPGLSDEK-------
          :   | |   |  | |            | | ||  |           |
FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNS
X           10        20        30        40        50        60

   70        80        90       100       110       120       130
--LNLTIQNDAYIPKYDSNGTSDIEQHDVNELNVFYLDAQKVPEGENNVNLTSSIDTALLEQPKIYTFFSS
      ||||      |   :  |  | | :|: :|:  |        ||  |  |    :|  |
VFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWT---LIDINGKTKSVFFEY
70        80        90       100       110       120       130

140          150       160       170       180       190       200
EFINNVNKPVQAALFVSWIQQVLVDFTTEANQKSTVDKIADISIVPYIGLALNIGNEAQKGNFKDALELLG
        ||| :|:                   | | |  || |:||          |||
NIREDISEYINRWFFVTITNNLNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSI
140          150       160       170       180       190       200

210          220       230       240
AGILLEFEP--------ELLIPTILVFTIKSFLGSSDNKNKVIKAINNA-------------------
                  :: |||| || || |  :| |||  |
FNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKDSPVGEILTRSKYNQNSKY
210          220       230       240       250       260       270       280

   250       260       270       280       290       300       310
LKERDEKWKEYYSFIVSNWMTKINTQFNKRKEQMYQALQNVNAIKTII------ESKYNSYTLEEKNELT
  ||  ||           :|       |            :                 |
INYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFY
290          300       310       320       330       340       350

320          330       340       350       360       370       380 X
NKYDIKQIENELNQKVSIAMNNIDRFLTESSISYLMKLINEVKINKLREYDENVKTYLLNYIIQHGSIL
|:  |        |       |        |           ||   |            ||   |
NTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVRKPYINLKLG
360          370       380       390       400       410       420 X

CNWQFIPKDEGWTE
430
```

```
> O <
O||O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-29.res made by bobryen on Thu 7 Nov 102 14:49:57-PST.

Query sequence being compared:US-09-910-186A-29 (1-1227)
Number of sequences searched:                        3
Number of scores above cutoff:                       3

    Results of the initial comparison of US-09-910-186A-29 (1-1227) with
        File :US08123975A.seq
```

```
Sequence Name        Description                                          Length  Score  Score  Sig.  Frame
                                                                                  Init.  Opt.
---------------------------------------------------------------------------------------------------------
1. US-08-123-975A-4   Sequence 4, Application U                            1338    53     412   0.69    0
2. US-08-123-975A-1   Sequence 1, Application U                            1338    53     412   0.69    0
                      ****  1 standard deviation below mean  ****
3. US-08-123-975A-6   Sequence 6, Application U                            1351    48     412  -1.04    0
```

```
1. US-09-910-186A-29 (1-1227)
   US-08-123-975A-4  Sequence 4, Application US/08123975A

Initial Score          =     53    Optimized Score   =   412   Significance  =  0.69
Residue Identity       =    41%    Matches           =   499   Mismatches    =  633
Gaps                   =     64    Conservative Substitutions

                  50          60  X      70          80          90         100         110
     TTATTCTTTGTCGCTCCGAGTCAAGCTCAACAGAACGATAT-TAACACACCTAAAGAGATTGACGATAC
         ||    |||   |||||| |  |||||| | ||      |        ||| | |||||||| |   |
                  CTCGAGCCATGGCTGCTGCTGCTGCTCGTCTGTCTACCTTCACTGAATACATCAAGAACAT
                  X         10          20          30          40          50

                 120         130         140         150         160         170         180
     TACCAACCTAAACAACAACTACCGGAACAACTTGGATGAGGTTATTTTGGATTACAACTCACAGACCATCCC
        ||    |     |||  |    |||| | |    |||   ||||| |||  |||||| ||| ||  ||||
           CATCAATAACCTCCATCCTGAACCTGGCTAC---GAATCCAATCACCTGATCGACCTGCTCGCTACGCTTC
              60          70          80          90         100         110         120

                 190         200         210         220         230         240         250
     TCAAATTTCCAACCGTACCTTAAACACTCTTGTCCAAGACAAC--TCCTACGTTCCAAGATACGATTCTAAC
         |||| || |  |||   | |   |||  ||  ||| |||    | | ||| |||| ||| |  ||| |||
     CAAAATCAACAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCT--G
        130         140         150         160         170         180         190

                 260         270         280         290         300         310         320
     GGTACCTCAGAGATCGAGGAGTAGTATGATGTTGTTGACT-TTAACGTCTTTTTCTATTTGCATGCCCAGAAGGT
         |   ||   |   | || |   |   |  |     |     || ||      |   |  ||| ||||| |
     GAATCTTCCAAAATCGAAG---TTATCCTGAAGAATGCTATCGTATTCAACTTCTATG-TACGAAAACTTC
        200         210         220         230         240         250

                 330         340         350         360         370         380         390
     GCCAGAAGGTGAAACCAACATCTCATTGACTTCTTCCATTGATACCGGCCTTGTTGGAAGAGTCCAAGGATAT
         ||  |||     | | || |||   | |   |||||| ||   |||   ||| |||| || || |||| |
              TCCACCTCCTTCTGAATCCGTATCCCGAAATACTTCAACT---CCATCTCTGACAATGAATACACCAT
        260         270         280         290         300         310         320

                 400         410         420         430         440         450         460         470
     CTTCTTTTCTTCGGAGTTTATCGATACTATCAACAAGCCTGTCAACGCCGCTCGTCGTTCATTGATTGGATTAG
         || ||| |  | ||| ||  ||| || |  |||   |  | |    ||| ||   ||| || ||   |||||
     CATCAACTGCATGGAAAACAATTCTGGTTGAAAGTATCTCGAACTACGGTGAAATCAT--CTGGACTCTG
        330         340         350         360         370         380         390

                 480         490         500         510         520         530         540
     CAAGGTCATCA-GAGATTTTACCACTGAAGCTACTCAAAAGTCCACTGTTGAT-AAGATTGCTGACATCTCT
         |||| ||||  |||| || | |  || ||   |  |||| | | |  ||||    || ||| |||| |||
     CAGGACACTCAGGGAAATCAAACAGCGTGTTGTATTCAAATCAAATACTCTCAGATGATCAACATCCTCGAC----
        400         410         420         430         440         450         460

                 550         560         570         580         590         600         610
     TTGATTGTCCCCTATGCGCGGTCTTGCTTTGAACATCATT-ATTGAGGCAGAAAGGGTAACTTTGAGGAGG
        ||  ||| || | |||  |  | ||||  || |||  ||   | ||| ||||| | ||| |||| |||||
     TACATCAATCGCTGGATCTTCCGTTACCATACCAACCACCAACATCGTCTCAGAATTACTACACATCAACGGC
        470         480         490         500         510         520         530

                 620         630         640         650         660         670         680
     CTTTTGAATTGTGTGGGAGTTGGTATTTTGTTGGAGTTTGTTCCAGAACTTACCATTCCTGTCATTTTAGTTT
        ||  ||| |||   || | || ||| | |  || || || | |  ||  ||  ||||  |  | |||  |||
     CGTCTGATCGACCAGAAACCGATCTCCAACTGGGTAACATCCA-CGCTTCTAATAACATCATGTTCAAACT
        540         550         560         570         580         590         600

                 690         700         710         720         730         740         750
     TTACG---ATCAAGTCCTACATCGATTCATACGAGACAAGAATAAAGCAATTAAAGCTATTAACAACTCCT
         ||| |   |  ||||  || |||   | |  |||||  |
```

2. US-09-910-186A-29 (1-1227)
US-08-123-975A-1 Sequence 1, Application US/08123975A

```
Initial Score    =  53        Optimized Score   = 412        Significance         = 0.69
Matches          = 41%        Matches           = 499        Mismatches           = 633
Residue Identity =  64        Conservative Substitutions = 64        Gaps         = 0
```

```
       1100      1110      1120      1130      1140         1150      1160
     CGATAACCACGTTAAGAGCGATCTGCTGAACTACATTCTCGACCACAG--ATCAATC-CTGGGAGAGCAGAC
      | |      |  |||| |             | || |  |||    |  |||  || | || ||     |
     GGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAAT
           1040      1050      1060      1070      1080      1090      1100

        1170      1180      1190      1200      1210      1220      X
     AAACGAGCTGAGTGATTTGGTTACTTCCACTTTGAACTCCTCCATTCCATTTGAGCTTTCTTAA
      ||      ||  ||   || ||    ||||   || | |   ||     |  ||       |
     GAAATCCAAGAACGACCAGGGTA---TCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGA
         1110      1120         1130      1140      1150      1160  X   1170

     TATCGGTTTCAT
          1180

3. US-09-910-186A-29 (1-1227)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    48  Optimized Score  =   412  Significance = -1.04
Residue Identity =   41%  Matches          =   483  Mismatches   =   620
Gaps             =    68  Conservative Substitutions           =     0

             80        90       100       110       120       130       140
     ACAACGAGAACGATATTAACACACCTAAAGAGATTGACGATACTACCAACCTAAACAACAACTACCGGAA-C
                         |   ||    | |   || || |    | ||| ||||| | |  || ||| |
                         ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                         X        10        20        30        40        50

           150       160       170       180       190       200       210
     AACTTGGATGAGGTTATTTTGGATTACAACTCACAGACCATCCCTCAAATTTCCAACCGTACCTTAAACACT
       | |     ||   |   |    |  | ||  | |   |     | ||  |  ||   |||     ||  |
     TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATAC----GACGGT
           60        70        80        90       100       110           120

         220       230       240       250       260       270
     CTTGTCCAAGACAACTCCTACGTTCCAAGATACGATTCTAACGGTACCTCAGAGATCGAGG------AGTAT
      |||  |   |  ||    ||      | |      |||  || || |||  |||||   |      || ||
     GTTGAACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAAT
            130       140       150       160       170       180       190

   280       290       300       310       320       330       340       350
     GATGTTGTTGACTTTAACGTCTTTTTCTATTTGCATGCCCAGAAGGTGCCAGAAGGTGAAACCAACATCTCA
      |     |   ||| |||  | | |||   | |  | | | |       | | |   | | ||   |   ||
     CAGAACATCATCTTCAACTCCGTATTC--CTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACA
          200       210         220       230       240       250       260

           360       370       380       390       400       410       420
     TTGACTTCTTCCATTGATACCGCCTTGTTGGAAGAGTCCAAGGATATCTTCTTTTCTTCGGAGTTTATCGAT
        ||  |    ||  | |    | |     | || | ||     ||| ||   |    | ||  || |  |
     AGAACGAC-GGTATCCAGAATTACATCCACAATGAATACA---CCATCATCAACTGCATGAAGAATAACTCT
          270        280       290       300          310       320       330

         430       440       450       460       470       480       490
     ACTATCAACAAGCCTGTCAACGCCGCTCTGTTCATTGATTGGATTAGCAAGGTCATCAGAGATTTTACCACT
       |   || |   |  ||  ||     |   ||||        | | | |  ||| | |  |    |   ||
     GGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCT
            340       350       360       370       380       390       400

       500       510       520       530       540       550       560
     GAAGCTACTCAAAAGTCCACTGTTGATAAGATTGCTGACATCTCTTTGATTGTCCCCTATGTCGGTCTTGCT
     | |       || |   ||    |||  | ||  ||||          ||    |  |   | | ||||  |
     GTATTCTTCGAATACAACATCCGTGAAGACATCTCTGA----------ATACATCAATCGCTGGTTCTTCGT
          410       420       430       440                 450       460

     570       580       590       600       610       620       630
     TTGAACATCATTATTGAGGCAGAAAAGGGTAACTTTGAGGAGGCTTTTGAATTGTTGGGAGTTGGTATTTTG
     |  | |||||  | | |     | || | |||  |  |         | ||    ||| |  |  ||
     T--ACCATCACCAATAACCTGAACAATGCTAAAATCTACATCAACGGTAAA---CTGGAATCTAATACCGAC
          470       480       490       500       510          520       530

   640       650       660       670       680       690       700       710
     TTGGAGTTTGTTCCAGAACTTACCATTCCTGTCATTTTAGTTTTTACGATCAAGTCCTACATCGATTCATAC
      |  |     | |  ||| ||| |  |   |      |  | || |   |  |     ||||||||     |
     ATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACC
           540       550       560       570       580       590       600

             720       730       740            750       760       770
     GAGAACA--AGAATAAAGCAATTAAAGCTATTAA-----CAACTCCTTGATCGAAAGAGAGGCTAAGTGGAA
      ||  ||   | || ||  | ||     | || |      ||||   | |    || |  |   ||  || |
     CAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAA-CGGTA
         610       620       630       640       650       660        670

      780       790       800       810            820       830       840
     GGAAATCTACTCATGGATTGTATCAAACTGGCTTACT--AGAATTAACACTCAATTTAACAAGAGAAAGGAG
       | ||| | || |     | ||  | |||    |||   |   |||  | |   |  |||| | | |  |
     CAAGATCCAGTCTTACTCCGAAT--ACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATAC
        680       690         700       710       720       730       740

      850       860       870       880       890       900       910
     CAAATGTACCAGGCTCTGCAAAACCAAGTCGATGCTATCAAGACTGCAATTGAATACAAGTACAACAACTAT
      | |||| | | |||  | || |  || ||  |   |||||       |  || |    |       |
     TATATGTTCAATGCT-GGTAACAAGAACTC--TTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATC
        750        760       770         780       790       800       810

    920       930       940       950       960                970       980
     ACTTCCGATGAGAAGAACAGACTTGAATCTGAATACAATATCAAC---------AACATTGAAGAAGAGTTG
         |   |   ||  |||  |   | ||| ||||||  | | ||          |||| |  ||| ||||
     CTGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTC
         820       830       840       850       860       870       880

                990          1000      1010      1020      1030      1040
     AACA-----AGAAAGT----TTCTTTGGCTATGAAGAATATCGAAAGATTTATGACCGAATCCTCTATCTCT
     | ||      | || |     |||  | | || ||  ||  |     |  ||     || | |     |
     ATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTG
       890       900       910       920       930       940       950

       1050      1060      1070      1080      1090      1100      1110
     TACTTGATGAAGTTGATCAATGAGGCCAAGGTTGGTAAGTTGAAGAAGTACGATAACCACGTTAAGAGCGAT
      ||||  | ||  |||   | ||       ||    |  |  ||| | | | | ||  | |   | |    |
     GACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGAAAAGCTT
     960       970       980       990      1000      1010      1020

     1120      1130      1140      1150      1160      1170      1180
     CTGCTGAACTACATTCTCGACCACAGATCAATCCTGGGAGAGCAGACAAACGAGCTGAGTGATTTGGTTACT
      | |||  || |  ||||     | ||  ||  ||   | | ||  || |  |    |   |    |
     TTCCTG-GCTCCGATCTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAA--TACGACGAACAG
  1030       1040      1050      1060      1070      1080        1090

   1190      1200      1210      1220      X
     TCCACTTTGAACTCCTCCATTCCATTTGAGCTTTCTTAA
      | || |     | |    | |  ||  ||     | ||
     CCGACCTACTCTTGCCAGCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGG
   1100      1110      1120      1130      1140      1150
```

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> O <
O| |O   IntelliGenetics
> O <
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-29-inv.res made by bobryen on Thu 7 Nov 102 14:50:14-PST.

Query sequence being compared:US-09-910-186A-29' (1-1227)
Number of sequences searched:          3
Number of scores above cutoff:         3

Results of the initial comparison of US-09-910-186A-29' (1-1227) with:   complement
        File : US08123975A.seq
```

```
Sequence Name    Description                                              Length  Init.  Opt.   Sig.  Frame
                                                                                  Score  Score  Score
-----------      ---------------------------------------------------      ------  -----  -----  ----  -----
1. US-08-123-975A-4  Sequence 4, Application U                            1338     36    455    0.87    0
2. US-08-123-975A-1  Sequence 1, Application U                            1338     36    455    0.87    0
3. US-08-123-975A-6  Sequence 6, Application U                            1351     32    372   -0.87    0
```

```
1. US-09-910-186A-29' (1-1227),
US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score       =   36    Optimized Score        =   455    Significance  =   0.87
Residue Identity    =   42%   Matches                =   549    Mismatches    =   651
Gaps                =          Conservative Substitutions =  98  Gaps         =     0
```

```
                    X         10        20        30        40
          TTAAGAAAGCTCAAATGGAATGGAGGAGTTCAAAGTGGA------AGTAA
CGTCGCGCTGCTCTACCTTCACTGACATACATCAAGAGACATCATCAATACCTCCATCCTGCAACCTGCGCTACGAA
          20        X         40        50        60        70        80

                    50        60        70        80        90       100       110
CCAAATCAC---TCAGCTCGTTTGTCTGCTCTCCCAGGATTGATCTGGTCGGAGAATGTAGTTC-AGCAG
          ||||||    ||||| ||||| |||||  | |||   |||| |  ||  || || |
TCCAATCACCTGACCTGTCTCCGCTACGCTCCAAAATCAACATCGGTTCTAAAGTAACTTCGATCCG
90        100       110       120       130       140       150

                    120       130       140       150       160       170
ATCGGCTCTTAACGTGGT---TATCGTACTTCTTCAACTTACCAACCTTGGCCTCAT--TGATCAACTTCATC
          ||||       ||| |||    ||  |||  |||     ||| |||||||   |||| |||
ATCGGACAAGAATCAGAGCTGTTCAATCTTCAATCTGAATCTCCAAAATCGAAGTTATCCTGAAGAAATGCTATC
160       170       180       190       200       210       220       230

                    180       190       200       210       220       230       240       250
AAGTAAGAGATAGAGGATTCGGTCATAAATCTTTCGATATTCTTCATAGCCAAAGAAACTTTCTTGTTCAAC
          ||||  |  |||    ||| ||  |||||  |  ||||   || |||||    |||||   |||
GTATACAACTCTATGTACGAAAAACTTCTCCACCCTTCTGGATCCGTATCCCGAAAATACTTCAACTCCATC
240       250       260       270       280       290       300

                    260       270       280       290       300       310       320
TCT-TCTTCAAAGTGTTGATATTGTATTCAG-ATTCAAGTCGTGTTCTTCTCATCGGAAGATAGTTGTTGT
          |||| ||| ||  |  ||||  ||| ||||  |  || |||  ||||||||    |||||
TCTCTGAACAATGAATACACCATCAACTGCATCATGATGAAAACAATTCTCGGT--TGGAAGTATCTCTGAACT
310       320       330       340       350       360       370

                    330       340       350       360       370       380
AC-TTGTATTCAATTGCAGTCTTGATAGCATGCAGCTTGGTTTTGCAGACCTGGTA--CATTTGCTC-----
          || ||| |||  |||  ||| |||   |||   ||  |||| |||  |||||||    |||||||
ACGGTGAAATCATCTGGACTCTGCGAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGA
380       390       400       410       420       430       440

                    390       400       410       420       430       440
--------CTTCTCTTGTTAAATTGAGTGTTAATTCTAGTAAGGCCAGTTGATACAAATCCATGAGTAGAT-TT
          ||||| |||||     ||||  ||  ||||  | ||||||   || || ||  |||| |||| ||
TGATCAACATCTCTGACTACGAAAAAGCTCCTCTGGATCTTCGTTACCATCACCAACCAATCCTGAATAACTCCA
450       460       470       480       490       500       510

                    450       460       470       480       490       500       510       520
CCTTCCACTTAGCCTCTTCCTTCGATCAAGGAGTGTTAATAGCTTGAAGTCTTAATTGCTTATTCTTGTCTCGTATG
          ||||      |||||  ||  |||||  ||  ||||| ||||  || ||| |  ||
AAATCTACATCAAGGACGGCCGTCCGATCGACCAGAAACCGATCTCAAATCTGGGTAACATCCCACGCTTCTAATA
520       530       540       550       560       570       580

                    530       540       550       560       570       580       590
AATCGATGTAGGACTTGATCGTAAAACTAAAATGACAGGAATGGTAAGGTTCTGGACAAACTCCAACAAAA
          |  |  |  ||||      ||||||   |    |    |  ||   |  | ||||||  |||| |||||
ACATCATGTTCAAACTGGACG-----GTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCT
590       600       610       620       630       640       650

                    600       610       620       630       640       650       660
TACCAACTCCCAACAATTCAAACAGGATCACTCCTCTCAAGTTACCCTTTTCTGCCTCAATAATGATGTTCAAAGCAA
          |||    |||||||  ||||||||| |||  |   ||   | |   ||  ||||  |||| ||||||
GTTCGACAAGAACTGAACGACCAGTCAACCAGTCAACAACCAGCAACCAGTCCAATTCTCAATTCTGGTATCCT
600       610       620       630       640       650       660
```



```
100-
  -
  -
  -
N -
U 50-
M -
B -
E -
R -
  -
O -
F 10-
  -
  -
S 5-
E -
Q -
U -
E -
N -
C -
E -
S 0-------------------------------------------------------------------
        |  | | | | | | | |  | | | | | | | |  | | |  | |
SCORE 0  4  8  12 16 20 24 28 32 36
STDEV    -9 -8 -7 -6 -5 -4 -3 -2 -1  0
```

```
                PARAMETERS

Similarity matrix     Unitary    K-tuple              1         4
Mismatch penalty      1          Joining penalty      5.00      30
Gap penalty           5.00       Window size          0.33      500
Gap size penalty      0.33
Cutoff score          1
Randomization group   0
```

```
              SEARCH STATISTICS

Scores:      Mean    Median     Standard Deviation
             34      33         2.31

Times:       CPU                Total Elapsed
             00:00:00.00        00:00:00.00

Number of residues:              4027
Number of sequences searched:       3
Number of scores above cutoff:      3
```

```
The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

TCCAATCACCTGATGACCTGTCTCGCTACGCTTCCAAATCAACACATCGGTTCTTAAAGTTAACTTCGGATCCG
          90   100   110   120   130   140   150
ATCGGCTTCTTAACGTGGT---TATCGTACTTCTTCAACTTACCAACCTTGGCCTCAT--TGATCAACTTCATC
        160   170   180   190   200   210   220   230
ATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCAAAATCGAAGTATCCTGAAGAATCGTATC
  180   190   200   210   220   230   240   250
AAGTAAGAGATAGAGAGGATTCGGTCATAAAATCTTTCGATATTCTTCATAGCCAAAGAAACTTTCTTGTTCAAC
                240   250   260   270   280   290   300
GTATACAACTCCATGTACGAAAACTTCTCCACCTCCCTTCTGGATCCGTATCCGGAGTATCCTCAACTCCATC
        240   250   260   270   280   290   300

TCT-TCTTCAATTGCAGTCTGATAGCATCGATCGACTTGGTTTCGCAGAGCCTGGTA--CATTTGCTC------
          310   320   330   340   350   360   370
TCTCTGAACAATGATACACCATCATCAACATCTGGT--TGGAAAGTATCTCTGAACT
260   270   280   290   300   310   320

AC-TTGTATTCAATTGCAGTCTGGACTCTGCGAGGACCACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTTCTCAGA
          330   340   350   360   370   380
ACGGTGAAATCATCTGGACTCTGCGAGGAAATCAAACAGCGTGTTGTATTCAAATACTTCTCAGA
        330   340   350   360   370   380

CA-------------TCATACTCCCTGCGATCT-CTGAGGTACCGTTAGAATCCGTATCTTGGAACGTA
                          390   400   410   420   430   440
CTTCTCTTGTTAAATTGAGTGTTAATTCTAGTAAGCCAGTTGATACAATCCATGAGTAGAT-TT
          390   400   410   420   430   440

TGATCAACATCTCTGACTACATCGCTGAGATCTTCGTTCCATCACCAACAATCGTCTGAATAACTCCA
450   460   470   480   490   500   510

CAAAGAATACGTCTGGCTACCAGTCTCTCAGGCTGCGTGGTAGAAAAAGATCTTGTCGCTCTGGAAATCCC
1000   1010   1020   1030   1040   1050   1060

GGA------GTTGTCTTGGACAAGAGTGTTTAAGGTACGGTTGGAAATTTGAGGGTTGGTCTGTGAGTTGTAA
1070   1080   1090   1100   1110   1120   1130

2. US-09-910-186A-29' (1-1227), Application US/08123975A
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score   =   36   Optimized Score   =   455   Significance   =   0.87
Residue Identity =   42%   Matches   =   549   Mismatches   =   651
Gaps   =   98   Conservative Substitutions   =   0

```
      930       940       950       960       970       980       990

                          950       960        970       980       990
    CA-------------------TCATACTCCTCGATCT-CTGAGGTACCGTTAGAATCGTATCTTGGAACGTA
    ||                     || || |||   ||  ||  | |  | |    ||   ||| | ||
    CAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCC
   1000      1010      1020      1030      1040      1050      1060

         1000      1010      1020      1030      1040      1050      1060
    GGA-----GTTGTCTTGGACAAGAGTGTTTAAGGTACGGTTGGAAATTTGAGGGATGGTCTGTGAGTTGTAA
    |||     ||  |||    || |    | ||| | |      |||     ||||     ||   |  || ||
    GGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAA
 1070      1080      1090      1100      1110      1120      1130      1140

       1070      1080      1090      1100      1110        1120      1130
    TCCAAAATAACCTCATCCAAGTTGTTCCGGTAGTTGTTGTTTAGGTTGGTAGTA--TCGTCAATCTCTTTAG
        ||    |   |    | | ||  || ||   |||   | ||||   |  |  ||  |||| ||  ||
    AATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAA
         1150      1160      1170      1180      1190      1200      1210

       1140      1150      1160      1170      1180      1190      1200
    GTGTGTTAATATCGTTCTCGTTGTAGCTTGACTCGGAAGCGACAAAGAATAATTCTGAGTTGTTGACTCTAA
        |||  | ||   || ||   | | | |    ||| ||          | |||| |||| |      |
    ACTGGTTGCT-TCCAACTGGTACAATCGTCAGATCGAA-CGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAG
       1220       1230      1240      1250       1260      1270      1280

     1210      1220      X
    TACACAGACGTGGTGGGGCCAT
    | ||     || |  |     |
    TTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAA
       1290      1300    X 1310      1320

3. US-09-910-186A-29’ (1-1227)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =      32  Optimized Score  =     372  Significance = -0.87
Residue Identity =     42%  Matches          =     450  Mismatches   =   528
Gaps             =      87  Conservative Substitutions            =     0

       200       210    X  220       230       240       250       260
    ATTCGGTCATAAATCTTTCGATATTCTTCATAGCCAAAGAAACTTTCTTGTTCAACTCTTCTTCAATGTTGT
                        ||    ||||    |||| | | || |    ||        |   ||  ||
                        ATGGCTTTCA---ACAAATACAATTCCGAAATCCTGAACAATATCATCCTGA
                        X       10           20        30        40

     270       280       290       300       310       320       330
    TGATATTGTATTCAGATTCAAGTCTGTTCTTCTCATCGGAAGTATAGTTGTTGTACTTGTATTCAATTGCAG
       |    ||   |||    | |||| ||      || |  ||   | || |  | ||| | |  |   | |
    ACCTGCGTTACAAAGACAACAATCTGATCGATCTGTCTG--GTTACGGTGCTAAAGTTGAAGTATACGACGG
   50        60        70        80          90       100       110

   340       350       360       370       380       390       400       410
    TCTTGATAGCATCGACTTGGTTTTGCAGAGCCTGGTACATTTGCTCCTTTCTCTTGTTAAATTGAGTGTTAA
    | ||||    |  |||  |     |   |  |||  || | | |  ||  |||    |||  |  ||||||
    TGTTGAACTGAATGACAAGAACCAGTTCAAACTG--ACCTCTTCCGCTAACTC----TAAGATCCGTGTTAC
  120       130       140       150         160       170           180

           420       430       440       450       460       470
    TTCTAGTAAGCCAGTTTGATACAATCCATGAGTAGATTTCCTTCCACTTAGCCTCTCTTTCGAT--------
    |   | | ||    |    | |||  |   | |      | |  |  ||  | |||   ||  |
    TCAGAATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAA
          190       200       210       220       230       240       250

          480         490       500       510       520       530
    ---CAAGGA--GTTGTTAATAGCTTTAATTGCTTTATTCTTGTTCTCGTATGAATCGATGTAGGACT-----
       |||| |     ||    ||  |||  | |   ||   |   |    || ||  |    | || |
    ATACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTC
    260       270       280       290       300       310       320

     540       550       560       570             580       590       600
    TGATCGTAAAAACTAAAATGACAGGAATGGTAAGTTCTG------GAACAAACTCCAACAAAATACCAACTC
    || | | || | ||  |    | | ||  |||   ||||      || | |  || |    || ||||| ||
    TGGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATC
  330       340       350       360       370       380       390       400

         610          620       630       640         650        660
    CCAACAATTCAAA---AGCCTCCTCAAAGTTACCCTTTTCTGCCTCAAT--AATGATGTTC-AAAGCAAGAC
       |   ||| ||   | | |||   |||  | |  |   | | |||||     | | |||   | ||  ||
    TGTATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCAC
          410       420       430       440       450       460       470

   670       680       690       700       710       720       730       740
    CGACATAGGGGACAATCAAAGAGATGTCAGCAATCTTATCAACAGTGGACTTTTGAGTAGCTTCAGTGGTAA
    | | |    | |||||   | |     || |||   |    | | |||| | | |  | || |  ||      |
    CAATAACCTGAACAATGCTAAAATCTACATCAACGGT----AAACTGGAATCT--AATACCGACATCAAAGA
        480       490       500       510           520         530

           750       760          770       780       790       800
    AATCTCTGATGACCTTGCTAA---TCCAATCAATGAACAGAGCGGCGTTGACAGGCTTGTTGATAGTATCGA
     |||  ||| |   | |||||   |  |||||      |    | || |||||      | ||| ||| | |
    CATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACA------TCGATCGTACCCA
  540       550       560       570       580       590             600

  810       820       830       840       850       860       870       880
    TAAACTCCGAAGAAAAGAAGATATCCTTGGACTCTTCCAACAAGGCGGTATCAATGGAAGAAGTCAATGAGA
         || |       || || || |||   |   | |||||  |   | ||   |    |  || | ||
    GTTCATCTG-------GATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAAC
      610              620       630       640       650       660       670

          890       900          910       920       930       940       950
    TGTTGGTTTCACCTTCTGGCACC---TTCTGGGCATGCAAATAGAAAAAGACGTTAAAGTCAACAACATCAT
     ||        |  |||  | ||   | |  |  |  |   | |   ||  || | | ||  |  | |  ||
    GGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAAT
           680       690       700       710       720       730       740

           960       970       980       990      1000      1010
    ACTCCTCGATCTCTGAGGTACCGTTAGAATCGTATCTTGGAACGTAGGAGTTGTCTTGGACAAGAG------
    |||    | ||  ||  |         | || ||  |   |  | || |    |||  |    | |
    ACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATCC
         750       760       770       780       790       800       810

         1020      1030      1040          1050      1060       1070
    -----TGTTTAAGGTACGGTTGGAAATTTGA----GGGATGGTCTGTGAGTTGTA-ATCCAAAATAACCTCA
          |||  |  |||     ||| | | |       |    | | ||  |||| |||    | ||  |||
    TGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTCA
       820       830       840       850       860       870       880

  1080      1090      1100      1110      1120      1130      1140      1150
    TCCAAGTTGTTCCGGTAGTTGTTGTTTAGGTTGGTAGTATCGTCAATCTCTTTAGGTGTGTTAATATCGTTC
    ||    |   ||    |  |     | ||      | |   | ||   |   ||     |   | |||   |
    TC---ATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACC
        890       900       910       920       930       940       950

          1160      1170      1180      1190      1200      1210      1220
    TCGTTGTAGCTTGACTCGGAAGCGACAAAGAATAATTCTGAGTTGTTGACTCTAATACACAGACGTGGTGGG
    | |   |  ||| |  | ||| |   || |     |    |  |       ||   | | ||| |  |
    TGGACTT--CTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGAAAA
      960         970       980       990      1000      1010      1020

        X
    GCCAT
    ||  |
    GCTTTTCCTGGCTCCGATCTCTGAT
     1030      1040      1050
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-30.res made by bobryen on Thu 7 Nov 102 14:37:36-PST.

Query sequence being compared:US-09-910-186A-30 (1-408)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

Results of the initial comparison of US-09-910-186A-30 (1-408) with:
     File :US08123975A.pep
```

```
Sequence Name    Description                                        Length  Init.  Opt.
                                                                            Score  Score  Sig. Frame
---------------------------------------------------------------------------------------------------
                 **** 1 standard deviation above mean ****
1. US-08-123-975A-2  Sequence 2, Application US/08123975A    850    171    276    1.16    0
                 **** 0 standard deviation from mean ****
2. US-08-123-975A-3  Sequence 3, Application US/08123975A    415     18    174   -0.55    0
3. US-08-123-975A-5  Sequence 5, Application US/08123975A    439     14    134   -0.59    0
```

```
1. US-09-910-186A-30 (1-408)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =    171    Optimized Score    =    276    Significance    =    1.16
Residue Identity =    40%    Matches            =    165    Mismatches      =    202
Gaps             =     8     Conservative Substitutions    =     32
```

```
          X        10        20        30        40        50        60        70
MAPPRLCIRVNNSELFFVASESSYNENDINTPKEIDDTNLNNNYRNNLDEVILDYNSQTIPQISNRTLNTL
     : : : ::|:|:|               :     :|||
APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENTESL
     X        10        20        30        40        50        60        70

          80        90       100       110       120       130       140
VQDNSYVPRYDSNGTSEIEEYDVDFNVFFYLHAQKVPEGETNISLTSSIDTALLEESKD-IFFSSEFIDTI
     :|||||           :     || :||:::||||::        : |
TDFNVDVPVYEKQPA--IKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIKTA
     80        90       100       110       120       130       140

         150       160       170       180       190       200       210
NKPVNAALFIDWISKVIRDFTTEATQKSTVDKIADISLIVPYVGLALNIIIEAEKGNPEEAFELLGVGILLE
     |:|: :||:: :    :|:::|  |||||||||||||||||  ::     |::|||  :|::|::|
NKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASILLE
     150       160       170       180       190       200       210

         220       230       240       250       260       270       280
FVPELTIPVILVFTIKSYIDSYENKNKAIKAINNSLIEREAKWKEIYSVWLTRINTQFFNKRKEQMYQA
     :|||:|||: :|||       ||||||||  :  | :::|:|: :||   || :||||||
FIPELLIPVVGAFLLESYID---NKNKIIKTIDNALTKNEKWSDMYGLIVAQWLSVTVNTQFYTIKEGMYKA
     220       230       240       250       260       270       280

         290       300       310       320       330       340       350
LQNQVDAIKTAIEYKYNNYTSDEKNRLESEYNINNIEEELNKVSLAMKNIERFMTESSISYLMKLINEAKV
     |:|:|||            ::        ::|||:|:|||::::||  |:|||||||||
LNYQAQALEEIIKYRYNIYSEKEKSNINIDF--NDINSKINEGINQAIDNINNFINGCSVSVYLMKKMIPLAV
     290       300       310       320       330       340       350

        360       370       380       390       400       410       420
GKLKKVDNHVKSDLLNYILDHRSIIGEQTNELSDLVTSINSSIPFELS
     ||:|| ||||| ::|       |:::|
EKLLDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEIL
     360       370       380       390       400       410       420
```

```
2. US-09-910-186A-30 (1-408)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =    18     Optimized Score    =    174    Significance    =   -0.55
Residue Identity =    9%     Matches            =    36     Mismatches      =    330
Gaps             =     2     Conservative Substitutions    =     26
```

```
          X        10        20        30        40        50
MAPPRLCIRVNNSELFFVASESSYNENDINTPKEIDDTNLNNNYRNNLDEV
                                                   :
SNHLIDLSRYASKINIGSKVNFDPIDKNQLFNLESSKIEVILKNAIVFNSMYENFSTSEWIRIPKYFNSI
     10        20  X     30        40        50        60        70

          60        70        80        90       100       110       120
ILDYNSQTIPQISNRTLNTLVQDNSYVPRYDSNGTSEIEEYDVDFNVFFYLHAQKVPEGETNISLTSSIDT
     :              |                   :|||
SLNNEYTIINCMENNSGWKVSLNYGEIIW-TLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNS
     80        90       100       110       120       130       140
```

```
                                              Mean    Median
Scores:                                        67      15
                                                              Standard Deviation
                                                                     89.51

Times:             CPU                                              Total Elapsed
                   00:00:00.00                                      00:00:00.00

Number of residues:                           1704
Number of sequences searched:                    3
Number of scores above cutoff:                   3
```

```
SEARCH STATISTICS
```

```
                 PARAMETERS

Similarity matrix      PAM-150    K-tuple                 1
Threshold level of sim.   16%    Joining penalty         20
Mismatch penalty           1     Window size            408
Gap penalty             5.00
Gap size penalty        0.05
Cutoff score               1
Randomization group        0
```

```
100-

      -
 50-  -
      -
      -
      -
 N    -
 U    -
 M    -
 B    -
 E    -
 R 10-|       |       |       |       |       |       |
      -
 O    -
 F  5-|
      -
 S    -
 C    -
 O    -
 R    -
 E    -                                                            *
 S  0-|-------|-------|-------|-------|-------|-------|-------|-------|
       **
SCORE 0    19      38      57      76      95     114     133     152     171
STDEV 0     0
```

```
The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
             130       140       150       160       170       180       190
ALLEESKDIFFSSEFIDTINKPVNAALFIDWISKVIRDFTTEATQKSTVDKIADISLIVPYVGLALNIIIEA
             :|              : |:                   :|         : |
KIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKD
     150       160       170       180       190       200       210

 200       210       220       230       240       250       260
EKGNFEEAFELLGVGILLEVPELTIPVILVFTIKSYIDSYENKNKAIKAINNSLIEREAKWKEIYSWIVSN
         : :|                      |  |:                        :||
FWGDYLYQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTINIYLNSSLYRGTKFIIKKYASGNKD
 220       230       240       250       260       270       280       290

 270       280       290       300       310       320       330       340
WLTRINTQFNKRKEQMYQALQNQVDAIKTAIEYKYNNYTSDEKNRLESEYNINNIEEELNKKVSLAMKNIER
        ::|              :||                    : |     :|||
NIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNL-SQVVVMKSKNDQGITNKCKMNLQDN
 300       310       320       330       340       350       360

 350       360       370       380       390   X   400
FMTESSISYLMKLINEAKVGKLKKYDNHVKSDLLNYILDHRSIIGEQTNELSDLVTSTLNSSIPFELS
|:|           |||
NGNDICFGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL
 370       380       390       400       410   X
```

3. US-09-910-186A-30 (1-408)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

```
Initial Score     = 14     Optimized Score    = 134     Significance  = -0.59
Residue Identity   = 9%     Matches            = 246     Mismatches    = 15
Gaps               = 2      Conservative Substitutions = 29
```

```
 100       110       120       130       140       150       160
DFNVFFYLHAQKVPEGETNISLTSSIDTALLEESKDIFFSSEFIDTINKPVNAALFIDWISKVIRDFTTEAT
                                  FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVIDGVELNDKNQFKLTSS
                                  X         10        20        30        40        50

 170       180       190       200       210       220       230       240
QKSTVDKIADISLIVPYVGLALNIIIEAEKGNFEEAFELLGVGILLEVPELTIPVILVFTIKSYIDSYENK
                                            : |                 :|:
ANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRG--NRIIWT
     60        70        80        90        100       110       120

 250       260       270       280       290       300       310
NKAIKAINNSLIEREAKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDAIKTAIEYKYNNYTSDEKN
   |:|                   ||:
LIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG
     130       140       150       160       170       180       190

 320       330       340       350       360       370       380
RLESEYNINNIEEELNKKVSLAMKNIERFMTESSISYLMKLINEAKVGKLKKYDNHVKSDLLNYILDHRSIL
        :||                :|
DIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPV
 200       210       220       230       240       250       260

 390       400    X
GEQTNELSDLVTSTLNSSIPFELS
||
GEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVR
     270       280       290       300       310
```

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O| |O   IntelliGenetics
 > O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-31.res made by bobryen on Thu 7 Nov 102 14:50:45 PST.

Query sequence being compared: US-09-910-186A-31 (1-1233)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-31 (1-1233) with:
   File : US08123975A.seq

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-08-123-975A-4	Sequence 4, Application U	1338	51	427	0.58	0
2. US-08-123-975A-1	Sequence 1, Application U	1338	51	427	0.58	0
**** 1 standard deviation below mean ****						
3. US-08-123-975A-6	Sequence 6, Application U	1351	45	328	-1.15	0

1. US-09-910-186A-31 (1-1233)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score   = 51   Optimized Score   = 427   Significance = 0.58
Residue Identity = 43%   Matches   = 518   Mismatches   = 599
Gaps   = 84   Conservative Substitutions

```
                   X        10        20        30        40        50
              ATGGCCAAAAATACCGGTAAATCTGAACAGTGTATTATTGTTAATAAT-GAG
              |||  ||  ||  ||   ||              ||  ||    ||
CTAAAGTTAACTTCGATCCGATCGACAGAAT-CAGATCCAGCTGTTCAATCTGAATCTTCCAAAATCGAA
140       150       160       170       180       190       200

           60        70        80        90       100       110
GATTTATTTTCATAGCTA----ATAAAGATAGTTTTTCAAAAGATT---TAGTAAAGCAGAAACTATAGC
     ||  ||             ||||    ||         |||       |||
GTTATCCTGAAGAATGCTATCGTATCCTATGTACGAAAACTTCCCACCTCTCTGGATCCGTATC
210       220       230       240       250       260       270       280

          120       130       140       150       160       170       180
ATATAATACACAAAAT--AATACTATAGAAAATAATTTTCTATAGATCAGTTGATTTTAGATAATGAT--T
||||               ||  ||  ||   ||              ||       ||   ||
CCGAATACTTCAACTCCTCTGACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGT
290       300       310       320       330       340       350

          190       200       210       220       230       240       250
TAAGCAGTGGCATAGACTTACCAAATGAAAACACAGAAACCATTACAAATTTGACGACATAGATATCCCTG
|| ||               ||  ||||   ||   ||      ||      ||
TGGAAAGTATCTCGAACTAC--GGTGAAATCATCTGGACTCTGCAGGACACTCGAGGAAATCAAAACAGCGTG
360       370       380       390       400       410       420

          260       270       280       290       300       310       320
TGTATATTAAACAATCGCTTTAAAAAAAATTTTGTGGATGGAGATAGCCTTTTTGAATATTTACATGCTC
|| ||           ||    |||||||                ||
TTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACACATCAATCG-CTGGATCTTCGTTACCATCACC
430       440       450       460       470       480       490

          330       340       350       360       370       380       390
AAACATTTCCTTCTAATATAGAAAATCTACAACTAACGAATTC---ATTAAATGATGCTTTAAGAAATAAT
|| ||||              ||  |||      ||  || |      |||
AACAATGTCTGAATAACTCCAAAATCTACATCACACGGCCGTCGATCGACCAGAAACCGATCCCAATCTG
500       510       520       530       540       550       560

          400       410       420       430       440       450
AATAAAGTCTATACTTTT-------TTTTCTACAAAC--CTTGCTGAAAAAGCTAATACAGTTGTAGGTGC
|| ||                     ||  |||          ||
GGTAACATCCACCGCGTTCTAATAACATCATGTTCAAACTGGAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGG
570       580       590       600       610       620       630

          460       470       480       490       500       510       520
TTCACTTTTGTAAACTG--GGTAAAAGGAGTAATAGATGATTTTA-CATCTGAATCCACACAAAAAGTAC
|| ||              ||  |||||         ||           |||
ATCAAATACTTCAATCTGTTCGACAAAGAAATCTACACTCAATCTGGGGGTGAATTTATCAATCAAAATCAAGAAATCAAGGAAATCAAGGA
640       650       660       670       680       690       700       710

          530       540       550       560       570       580       590
TATAGATAAAGTTCAGATGTATCCATAATTATTCCCTATA-TAGGAC---CTGCTTTGAATGTAGGAAATG
||    ||        ||               ||       ||          |||
AATTCTGGTATCCTGAAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATCGTGAATCTG
720       730       740       750       760       770       780

          600       610       620       630       640
AAACAGCTAAAGAAA------ATTTTAAAAATG--------CTTTGAAATAGTAGGTGGA--GCCGCTAT
|| ||                    |||                |||
790
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

2. US-09-910-186A-31 (1-1233)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score   =   51   Optimized Score   = 427   Significance = 0.58
Residue Identity =   43%   Matches   = 518   Mismatches   = 599
Gaps   =   84   Conservative Substitutions =   0

3. US-09-910-186A-31 (1-1233)
US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score   =   45   Optimized Score   =   328   Significance   =   -1.15
Residue Identity   =   40%   Matches   =   367   Mismatches   =   501
Gaps   =   33   Conservative Substitutions = 0

```
                                                                        CCATC
```

```
> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-31-inv.res made by bobryen on Thu 7 Nov 102 14:51:01-PST

Query sequence being compared: US-09-910-186A-31' (1-1233)
Number of sequences searched:                              3
Number of scores above cutoff:                             3

   Results of the initial comparison of US-09-910-186A-31 (1-1233) with:   Complement
   File : US0812397SA.seq
```

Sequence Name   Description   Length Init. Opt. Sig. Frame
                                                                                       Score Score
-------------   -----------   ------ ----- ----- ---- -----
1. US-08-123-975A-4   Sequence 4, Application U   1338   49   446   0.67   0
2. US-08-123-975A-1   Sequence 1, Application U   1338   49   446   0.67   0
                      **** 1 standard deviation below mean ****
3. US-08-123-975A-6   Sequence 6, Application U   1351   36   322 -1.07   0

1. US-09-910-186A-31' (1-1233)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score   =   49   Optimized Score   =   446   Significance =   0.67
Residue Identity =   42%   Matches   =   522   Mismatches   =   640
Gaps   =   Conservative Substitutions =   78
```

```
                  20         30       X 40        50         60         70         80
         AGATCAAAATGTATAACTGTCTTTTAGGTGTCTATTAACTTTTGATTTTAGAATATTTACTTCATCAAGTAAA
                                      CTCGAGCCATGGCTCGTCGCTG-TCTACCTTCACTGAATACATCAAGAACA
                                      X        10         20        30        40        50

          90        100        110        120        130        140        150
         TATAGTTCATTTGATCTATATACTCCAATAAAATCTCCTTAAGATATC-ATCAAAGTCTTTTAACTTTTT
         TCATCAATACCTCCATCCTGACGCTACGAACCTGGTGTATGATCGAACCTGATCGACCTGTCTCGCTACGGCTTCCA
                   60         70        80         90        100        110        120

         160        170        180        190        200        210        220        230
         TACAGGTAATGGAATCATTCTATTCATTAGAGTAGATATGATGAGAACATTGGTTTATAAAAATCATCTATATTGTT
         AAATCAACATCGGTTCTAAAGTTAACTCCGATCCGTGACCAAGAACAAGAAATCAGAT-CCAGCTGTTCAATCTGGAA
                   130        140        150        160        170        180        190

         240        250        260        270        280        290        300
         TATTGCTAAATTTATACTTTGATTAAGTTTATATCATTAATTCATTACATTCATTTATC
         TCTTCCAAAATCGAAGTTATCCTGAAG---AATGCTATCGTATACAACTCTATGT----ACGAAAAC
                   200        210        220        230        240        250

         310        320        330        340        350        360        370
         TTCTTCACTATATCTATTATGATCGTTCTATATTTTTTCTATTGCTTGTGTGATTGATTATTTTAAGCATT
         TTCTTCACCTCCTTCTGGATCCGTATCCCGAAATA--CTTCAACTCCCATCTCTCGAACAATGAATACA--
                   260        270        280        290        300        310        320

         380        390        400        410        420        430        440
         GTACAATTCTTTCTTTTTATTGTATAAAATTGAGTATTAACCGT--TGAGAGCCACTCGCGATACTATC-AAAC
         --CCATCAACTGCATGGAAAACAATCTCGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGAC
                   330        340        350        360        370        380        390

         450        460        470        480        490        500        510
         CATACATATCGTCCATTTTTGATCCCTTTTCTTTAAAGCATTTTAAAATTTCTTTAGCTGTTTCATTTCCTTTAT
         TCTGCAGGAGGACCACTCGAGGAAATCAAACAGCCGTGTTGTATTCAAAATACTCTCGAGATCAACAATCTCTGACTA
                   400        410        420        430        440        450        460

         520        530        540        550        560        570        580
         TTCCTACATATGATTCTAAATGTAAAAAATCCAACTATAGGTACAATAAGTTCTGGA------ATAAACTCCAT
         CATCAATCGCTGGATCTTCGTTACCATCCAACAATCGTCTGAAGATCCAAAATCTACATCACACGGCCG
                   470        480        490        500        510        520        530

         590        600        610        620        630        640        650
         TAAGATAGGCGGCTCCACCTATTTCAAAAGCATTTTAAAATTTCTTTAGCTGTTTCATTTCCTACATTCAA
         TCTGAGTCGACCAGAAACCGATCTCCAA--TCTGGTAACATCCACGCT-----TCTAATAACATCATGTTCA
                   540        550        560        570        580        590        600

         660        670        680        690        700        710        720
         AGCAGGTCCTATATAGGAATAATTATGGATACATCTGAAACTTTATCTATAGTACTTTTTTTGTGTGGATTC
         ||||||||  || |||||  ||| ||||| |||||  |||||| |||| ||| |
```

```
SCORE  0 -|
          |
          |
          |
          |
      5 -|
          |
          |
          |
          |
     10-|
          |
          |
          |
          |
     50-|
          |
          |
          |
          |
    100-|

N -|
U -|
M -|
B -|
E -|
R -|
  O -|
  F -|
  S -|
  E -|
  Q -|
  U -|
  E -|
  N -|
  C -|
  E -|
  S -|

                                  *
                                *
SCORE 0 -|  -|  -|  -|  -|  -|  -|  -|  -|  -|  -|  -|  -|  -|
       -5   5   11  16  22  27  33  38  44  49
STDEV  -4  -3  -2  -1   0
```

```
PARAMETERS

Similarity matrix      Unitary
Mismatch penalty       1
Gap penalty            5.00
Gap size penalty       0.33
Cutoff score           1
Randomization group    0

                       K-tuple        4
                       Joining penalty 30
                       Window size     500

SEARCH STATISTICS

Scores:        Mean      Median      Standard Deviation
               44        37          7.51

Times:         CPU                   Total Elapsed
               00:00:00.00           00:00:00.00

Number of residues:                  4027
Number of sequences searched:        3
Number of scores above cutoff:       3

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

2. US-09-910-186A-31' (1-1233)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score   = 49   Optimized Score = 446   Significance = 0.67
Residue Identity = 42%   Matches   = 428   Mismatches   = 522
Gaps   =   Conservative Substitutions = 78

```
   AACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCA-
 960       970       980       990      1000      1010      1020      1030

    1070      1080      1090      1100      1110      1120      1130
   CAACTGATCTATAGAAAAATTATTTTCTATAGTATTATTTTGTGTATTATATGCTATAGTTTCTGCTTTAGC
      ||| |   |||||||  | || |||    |   | |    |   |   |  | | || || | |
   -GGCTGGT--GTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCT-GTCTCAGGTAGTTG
               1040      1050      1060      1070      1080       1090

  1140      1150            1160      1170      1180      1190      1200
   TAAATCTTTTGAAAAACTA------TCTTTATTAGCTATGAAAAATAAATCCTCATTATTAACAATAATACA
   |||     |  || ||| |      | |   | |   ||| ||||| ||||  ||  |  ||||||  ||
   TAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGA-CAACAATGGTAAC
 1100      1110      1120      1130      1140      1150       1160

      1210      1220            1230  X
   CTGTTCAGATTTACCGGTAT------TTTTGGCCAT
       || | || | |||| |       ||   | ||
   GATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTC
1170      1180      1190      1200    X 1210      1220

3. US-09-910-186A-31’ (1-1233)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    36  Optimized Score =    322  Significance = -1.07
Residue Identity =    40%  Matches         =    385  Mismatches   =   492
Gaps             =    67  Conservative Substitutions          =     0

         310       320 X     330       340       350       360       370
   TCTTCTTCACTATATCTATTATATTGATCTTCTATTATTTTTTCTATTGCTTGTGATTGATTATTTAAAGCA
                       ||     ||  | | ||   || | |   | ||      || ||    | |
                       ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                       X       10        20        30        40        50

       380       390       400       410               420       430
   TTGTACATTCTTTCTTTTATTGTATAAAATTGAGTATTAAC--------CGTTGAGAGCCACTGCGATACT-
   |     |      |    ||   ||  |  ||  |  | ||         |||||     ||  || |  |
   TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
         60        70        80        90       100       110       120

     440       450       460           470       480       490       500
   -ATCAAACCATACATATCTGTCCATTTT----TGATCCCTTTTCTTTAAAGCATTGGATATCGTCATAATAA
    |   ||  | |   | | || ||   |    |  |||  |  || |||   ||  |   |  ||| ||| |
   AACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAA--GATCCGTGTTACTCAGAATCA
      130       140       150       160       170         180       190

       510       520       530       540       550       560       570
   TATGCCCTTTATTTCCTACATATGATTCTAATGTAAAAAATCCAACTATAGGTACAATAAGTTCTGGAATAA
    |    | |  |   || | |||   |  | |        |||  ||  |     |     | | | ||||
   GAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTA-----TCCCGAAATAC
      200       210       220       230       240       250            260

     580       590       600       610       620       630       640
   ACTCCATTAAGATAGCGGCTCCACCTATTTCAAAAGCATTTTTAAAATTTCTTTAGCTGTTTCATTTCCTA
   |       |  |   |||   |    ||| ||    || |    | |   || | | |||  | |      |
   A-------AGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAA
                270       280       290       300       310       320

   650       660       670       680       690       700       710
   CATTCAAAGCAGGTCCTATATAGGGAATAATTATGGATACATCTGAAACTTTATCTATAGTACTTTTTTGTG
   |  |    | | |  ||  ||  |   ||   |  |   |||||| |   | ||| |||      |     |
   CTCTGGTTGGAAGATCTCCATCCGCGGTA---ACCGTATCATCTGGACTCTGATCGATA------TCAACGG
    330       340       350          360       370       380

 720       730       740       750       760       770       780       790
   TGGATTCAGATGTAAAATCATCTATTACTCCTTTTACCCAGTTTACAAAAAGTGAAGCACCTACAACTGTAT
   |     || || |  | || || | |||  | |   ||  |   |||       |  || | |   |||  |
   TAAGACCAAATCTGTATTCTTCGAATACAACAT---CCGTGAAGACATCTCTGAATACATCAATCGCTGGTT
 390       400       410       420          430       440       450

         800       810       820       830       840       850       860
   TAGCTTTTTCAACAAGGTTTGTAGAAAAAAAAGTATAGACTTTATTATTATTTCTTAAAGCATCATTTAATG
```

```
   | ||  || ||    |      || ||   || |  ||  || |        ||||     || ||||
   CTTCGTTACCATCACCAATAACCTGAACAATGCTAAAATCTACATCA----ACGGTAAACTGGAATCTAATA
  460       470       480       490       500           510       520

       870       880       890       900       910       920       930
   AATTCGTTAGTTGTAGATTTTCTATATTAGAAGGAAATGTTTGAGCATGTAAATATTCAAAAAGGCTATC--
       | | |     | ||     |  |||     ||  ||   | ||| |  | | |  |    |  |||
   CCGACATCA--AAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGA
    530         540       550       560       570       580       590

       940       950       960       970       980       990      1000
   TCCATCCACAAAAATTTTTTTTAAAGCAGATTGTTTAATATACACAGGGATATCTATGTCGTCAAAATTTGT
   ||   ||      || |   | |||      |   |  |  |||| |   | |||  |||  ||| ||
   TCGTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTC--CAATATCGAA
    600       610       620       630       640       650          660

    1010          1020      1030      1040      1050          1060
   AAATGGTTC----TGTGTTTTCATTTGGTAAGTCTATGCCACTGCTTAAATCA-----TTATCTAAAATCAA
    || ||| |    |    | | | |  | |   ||     ||| ||    | |     | || || ||  ||
   GAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAA
    670       680       690       700       710       720       730

 1070       1080       1090       1100       1110       1120       1130
   CTGATCTATA-GAAAAATTATTTTCTATAGTATTATTTTGTGTATTATATGCTATAGTTTCTGCTT------
        ||||| |   |||  |  |    || | | ||   |  |    | |  | | | || | ||
   GAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAA
  740       750       760       770       780       790       800       810

      1140      1150      1160      1170      1180      1190      1200
   TAGCTAAATCTTTTGAAAAACTATCTTTATTAGCTATGAAAAATAAATCCTCATTATTAACAATAATACACT
      || | || ||  ||| || | |   | |    || | |   |   || |    |  |||    |  |
   ATCCTGACTCGTTCCAAATACAACCAGAACTCTAAAT-ACATCAACTACCGCGACCTGTACATCGGTGAAAA
          820       830       840        850       860       870       880

    1210      1220      1230  X
   GTTCAGATTTACCGGTATTTTTGGCCAT
   |||||   |     | |  | |  |  |
   GTTCATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACAT
        890       900       910       920
```

```
> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-32.res made by bobryen on Thu 7 Nov 102 14:38:02-PST.

Query sequence being compared:US-09-910-186A-32 (1-410)
Number of sequences searched:                 3
Number of scores above cutoff:                3

Results of the initial comparison of US-09-910-186A-32 (1-410) with:
      File :US08123975A.pep
```

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig. Score	Frame
	**** 1 standard deviation above mean ****					
1. US-08-123-975A-2	Sequence 2, Application U	850	284	342	1.15	0
	**** 0 standard deviation from mean ****					
2. US-08-123-975A-3	Sequence 3, Application U	415	20	189	-0.56	0
3. US-08-123-975A-5	Sequence 5, Application U	439	14	132	-0.60	0

```
1. US-09-910-186A-32 (1-410)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =   284    Optimized Score  =   342    Significance    =   1.15
Residue Identity =   62%    Matches          =   252    Mismatches      =   125
Gaps             =    1     Conservative Substitutions   =            1              =    26

           X 10        20        30        40        50        60        70
MAKNTGKSEQCIIVNEDLFFIANKDSFSKDLAKAETIAYNTQNNTIENNFSIDQLILDNDLSSGIDLPNEN
              ||:||||||| |||: ||| :|:  |::  |:|||| |:|||| :||||||:|| |||||
APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSEN
X          10        20        30        40        50        60

           80        90       100       110       120       130       140
TEPFTNFDDIDIPVYIKQSALKKIIFVDGDSLFEYLHAQTFPSNIENLQLTNSLNDALRNNNKVYTFFSTNLV
              :  :::||| |||||| |||::||||||  :|||| |:|||  ||||| |||||||||
TESLTDF-NVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDRDISLTSSFDDALLFSNKVYSFSMDYI
70          80        90       100       110       120       130

          150       160       170       180       190       200       210
EKANTVVGASLFVNWVKGVIDDFTSESTQKSTIDKVSDVSIIIPYIGPALNVGNETAKENFKNAFEIGGAAI
             :|:  |:     ||| :||| |:|:||::|:|||||:|||||||||:|||||:||:||
KTANKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASI
140         150       160       170       180       190       200

          220       230       240       250       260       270       280
LMEFIPELIVPIVGFFTLESYVGNKGHIIMTISNALKKRDQKWTDMYGLIVSQWLSTVNTQFYTIKERMYNA
           |:|||||| | :||| ||||::: |: |:|||| ::|||:|:|||:||||:|||||   *
LLEFIPELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKA
210         220       230       240       250       260       270       280

          290       300       310       320       330       340       350       360
LNNQSQAIERKIIEDQYNRYSEEDKMNINIDFNDIDFKLNQSINLAINNIDDFINQCSISYLMNRMIPLAVKK
           ||:  |  |:|||:: | |:|||||::|| ::||:|| :|||:||:||||||:||:|:
LNYQAQALEPIIKYRVNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEK
290         300       310       320       330       340       350

          370       380       390       400  X    410
LKDFDDNLKRDLLEYIDTNELYLLDEVNILKSKVNRHLKDSIPPDLSLYT
           |||| |||||||  ||| |:|||||::  : | |  ||
LLDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSELLNNI
360         370       380       390       400  X    420
```

```
2. US-09-910-186A-32 (1-410)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =    20    Optimized Score  =   189    Significance    =  -0.56
Residue Identity =   10%    Matches          =    44    Mismatches      =   333
Gaps             =     4    Conservative Substitutions   =                             =    29

           X 10        20        30        40        50        60        70
MAKNTGKSEQCIIVNEDLFFIANKDSFSKDLAKAETIAYNTQNNTIENNFSIDQLILDNDLSSGIDLPNEN
          :                   |      |       |  ||  |||       |  ||
RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYF
X          10        20        30        40        50        60        70

           80        90       100       110       120       130       140
TEPFTNFDDIDIPVYIKQSALKKIIFVDGDSLFEYLHAQTFPSNIENLQLTNSLNDALRNNNKVYTFFSTNLV
            :  :  |      ::    :  ::       ::| :
NSISLNNEYIIINCMENNSGWKVSLNYGEIIWTLQDTQBIKQRV-VFKYSQMINISDYINRWIFVTITNNRL
80          90       100       110       120       130       140
```

```
  100-|

N   -|
    -|
U 50-|
M   -|
B   -|
E   -|
R   -|
    -|
O   -|
F 10-|
    -|
S   -|
E  5-|
Q   -|
U   -|
E   -|
N   -|
C   -| **                                                            *
E   -|
S   0-|_____|___
      0                                                                   284
SCORE 0    32    63    95   126   158   189   221   252   284
STDEV 0
```

```
                    PARAMETERS
Similarity matrix  PAM-150      K-tuple                1
Threshold level of sim.  16%
Mismatch penalty    1           Joining penalty       20
Gap penalty         5.00        Window size          410
Gap size penalty    0.05
Cutoff score        1
Randomization group 0

                 SEARCH STATISTICS
Scores:        Mean      Median      Standard Deviation
               106        15              154.18

Times:         CPU                    Total Elapsed
           00:00:00.00                00:00:00.00

Number of residues:          1704
Number of sequences searched:   3
Number of scores above cutoff:  3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                150       160       170       180       190       200       210
        EKANTVVGASLFVNWVKGVIDDFTSESTQKSTIDKVSDVSIIIPYIGPALNVGNETAKENFKNAFEIGGAAI
        :  ::  :|   |||   :   :|   ||   ||     |      ||       ||     ::|
        NNSKIYINGRLIIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGI
                150       160       170       180       190       200       210

                220       230       240       250       260       270       280
        LMEFIPELIVPIVGFFTLESYVGNKGHIIMTISNALKKRDQKWTDMYGLIVSQWLSTVNTQFYTIKERMYNA
        |:| ||  |   ::  ||  | | | || ||||||||||||||||||||||||||||||||||||||||||
        LKDFWGDYLQYDKPYYMLNLYDPNK---YVDVNNVGIRGYMYLKGPRGSVMTNIYLNSSLYRGTKFIIKKY
                220       230       240       250       260       270       280

                290       300       310       320       330       340       350       360
        LNNQSQAIEKIIEDQYNRYSEEDKMNINIDFDIDFKLNQSINLAINNIDDFINQCSISYLMNRMIPLAVKK
        :  : || |       |       |   ||| |:|  ||      |         |   |    |
        ASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVYVMKSKNDQGITNKCKM
                290       300       310       320       330       340       350

                370       380       390       400       410
        LKDFPDNLKRDLLEYIDTNELYLLDEVNILKSKVNRHLKDSIPFDLSLYT
        :|   |  |     ||    |  |   | |      |     |||||||||
        NLQDNNGNDIGFIGFHQFNNIAKIVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL
                370       380       390       400       X 410

3.  US-09-910-186A-32 (1-410)
    US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =    14   Optimized Score   =    132   Significance    =   -0.60
Residue Identity =    11%   Matches           =     32   Mismatches      =    239
Gaps             =     1   Conservative Substitutions =    18

                110       120       130       140       150       160       170
        DSLFEYLHAQTFPSNIENLQLTNSLNDALRNNNKVTFFSTNLVEKANTVVGASLFVNWVKGVIDDFTSEST
         | |    |     | | |     :| ||   | :::|::::    || |    :         |   |
        FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSS
                X       10        20        30        40        50

                180       190       200       210       220       230       240
        QKSTIDKVSDVSIIIPYIGPALNVGNETAKENFKNAFEIGGAAILMEFIPELIVPIVGFFTLESYVGNKGHI
            :||         ||  |    :|              ||
        ANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLI
                60        70        80        90       100       110       120

                250       260       270       280       290       300       310
        IMTISNALKKRDQKWTDMYGLIVSQWLSTVNTQFYTIKERMYNALNNQSQAIEKIIEDQYNRYSEEDKMNIN
         :         :   :|       |   |               |:
        DINGKTKSVFFEYNIREDISEYINRWFVTITNNLN-NAKIYINGKLESNTDIKDIREVIANGEIIFKLDGD
                130       140       150       160       170       180       190

                320       330       340       350       360       370       380
        IDFNDIDFKLNQSINLAINNIDDFINQCSISYLMNRMIPLAVKKLKDFDDNLKRDLLEYIDTNELYLLDEVN
        ||                |    |   |       |
        IDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVG
                200       210       220       230       240       250       260

        390       400
        ILKSKVNRHLKDSIPFDLSLYT
                       X
        EILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIV
                270       280       290       300
```

```
> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-33.res made by bobryen on Thu 7 Nov 102 14:51:25-PST.

Query sequence being compared:US-09-910-186A-33 (1-1314)
Number of sequences searched:            3
Number of scores above cutoff:           3

Results of the initial comparison of US-09-910-186A-33 (1-1314) with:
          File :US08123975A.seq
```

```
                                                             Init.  Opt.
Sequence Name    Description                          Length  Score  Score  Sig.  Frame
-----------------------------------------------------------------------------------------
1. US-08-123-975A-4  Sequence 4, Application U         1338   557    788   0.59   0
2. US-08-123-975A-1  Sequence 1, Application U         1338   557    788   0.59   0
                     **** 1 standard deviation below mean ****
3. US-08-123-975A-6  Sequence 6, Application U         1351   487    678  -1.14   0
```

```
1. US-09-910-186A-33 (1-1314)
   US-08-123-975A-4  Sequence 4, Application US/08123975A

Initial Score    =  557   Optimized Score        =  788   Significance =  0.59
Residue Identity =  61%   Matches                =  829   Mismatches   =   451
Gaps             =   71   Conservative Substitutions =  0
```

```
          10        20        30        40        50        60
GAATTCACGATGCTTACACTAACGACAAAATCCTGATCCTGT--ACTTCAACAAACTGTACAAAAAATC
                    |||  |||||  ||||| ||   |
          CTCGAGCCATGGCTCGTGCTGCTACCTTCACTGAATACATCAAGAACATC
                    10        20        30        40        50
          X

70        80        90       100       110       120       130       140
AAAGACAACTCTATCCTGACATCGTTACGAAAACAACAAATTCATCGACATCTCGGCTATGGTTCTAAC
ATCAATACCTCCATCCTGACAACCTGCGCTACGAACCTGATCGACCGTCTCGCGCTACGCTTCCAAA
      60        70        80        90       100       110       120

150       160       170       180       190       200       210
ATCTCTATCAACGGTGACGCTCACATCTACTCTTACTAACCGCAACCAGTTCGGTATCTACTCTTCTAAACCG
ATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCGTGTTCAAATCTGGAATCT
130       140       150       160       170       180       190

220       230       240       250       260       270       280
TCTGAAGTAAACATCGCTCAGAACAACAACGACACATCATCTACCAGGTCGTTACCGATCCTATCTCTCTATCTCTTC
TCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACCTCTATGTACGAAAAACTTCTCCACCTCCTTC
200       210       220       230       240       250       260

290       300       310       320       330       340       350
TGGGTTCGTATCCCGAAATACTTCAACAAAGTTAACCTGAACAACGAATACTATCATCGACTGCATCCGT
TGGATCCGTATCCCGAAATACTTCAACTCCAACTCTGAACATCTCTGAACAATAACACCATCAACTGCAT--G
270       280       290       300       310       320       330

360       370       380       390       400       410
AACAACAACTCTGGTGGAAAATCTCTCGAACTACAACAAAATCATCTGGACTCGCCAGGACACTGCTGGT
GAAAACAATTCGGTTGGAAAGTATCTCGTGGAAGTACGGTGAAATCATCTGGACTCGCCAGGACACTCCAGGAA
340       350       360       370       380       390       400

430       440       450       460       470       480       490       500
AACACCGAAAACTGGTTTTCAACTACATCCAGATGATCTCTATCTCTGACTACATTAATAAATGGGATCTTC
ATCAAACAGGCGTGTTGTATTCAAAATACTCCTGCAGATGATCAAACATCCTGACTACATCAATCGCTGGATCTTC
420       430       440       450       460       470       480

510       520       530       540       550       560       570
GTTACTACTCACTAACAACCGTCTGGTACTCTGTATCACATCACTCGTATTCTCTACATCACTTCCAATAAGAAAAATCT
GTTACCATCACCACCAACAATCGTCTGGAATAACGTTCACATCATTCACAAATCTACAACGCCGCCGTCTCGACCAGAAACCG
490       500       510       520       530       540       550

580       590       600       610       620       630       640
ATCTCTAACCTGGGTGACATCCACGTTTCTGACACACATCCTGTTCAAAATCGTTGGTTTGCAACGACAC--G
ATCTCCAATCTGGGTAACATCCACCGCTTCTAATAACAATCATGTTCAAAACTGGAACTGGTGCGTTGTCGTGCACACTCAC
560       570       580       590       600       610       620

650       660       670       680       690       700       710
CGTTACGTTGGTATCCGTACTTCAAAGTTTCCGACACTGGGTAAAATCGAAAATCGAAAACTCTGTAC
       |  |  |||   |||||||||||   |||| ||  ||  |||   |||||||  ||||||  |||||
560       570       580       590       600       610       620
```

```
100-|                                                           |
    |                                                           |
 N -|                                                           |
 U  |                                                           |
50-M|                                                           |
    |                                                           |
 B -|                                                           |
 E -|                                                           |
 R -|                                                           |
    |                                                           |
 O -|                                                           |
10-F|                                                           |
    |                                                           |
 S -|                                                           |
 5-E|                                                           |
 Q -|                                                           |
 U -|                                                        *  |
 E -|                                                           |
 N -|                                                           |
 C -|                                                   *       |
 E -|                                                           |
 S 0-|----------------------------------------------------------|
SCORE 0   62   124  186  248  309  371  433  495  557
STDEV     -9   -8   -7   -6   -5   -4   -3   -2   -1   0
```

```
                PARAMETERS

Similarity matrix   Unitary       K-tuple          1
Mismatch penalty    1             Joining penalty  30
Gap penalty         5.00          Window size      500
Gap size penalty    0.33
Cutoff score        1
Randomization group 0

              SEARCH STATISTICS

Scores:      Mean      Median     Standard Deviation
             533       488        40.41

               CPU                 Total Elapsed
Times:      00:00:00.00            00:00:00.00

Number of residues:           4027
Number of sequences searched:    3
Number of scores above cutoff:   3
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

2. US-09-910-186A-33 (1-1314)
US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score   =   557   Optimized Score   =   788   Significance   =   0.59
Residue Identity =   61%   Matches   =   829   Mismatches   =   451
                              Conservative Substitutions = 71   Gaps   =   0

3. US-09-910-186A-33 (1-1314)
US-08-123-975A-6 Sequence 6, Application US/08123975A

```
Initial Score   = 487    Optimized Score = 678    Significance = -1.14
Residue Identity = 54%    Matches         = 740    Mismatches   = 520
Gaps             = 90     Conservative Substitutions = 90       Gaps = 0
```

```
CTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGACAGCCGACCTACTCTTGCCAGC
1050      1060      1070      1080      1090      1100      1110

        1160      1170      1180      1190      1200
TCCAGAACAACAACG--------GTGGTAACATCGGTCGTCGCTGGTTTCCAC----TCTAACAACCTG
|-|-||||||             |-|||||||| ||||||||| ||| ||||   ||| ||| ||| |||
TGCTGTTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCGAAATCGGTATCGGTTCTACGAATCTG
1120      1130      1140      1150      1160      1170      1180

        1220      1230                 1240
GTTGCTTCTTC--ATGGTACTACAACAACATCCG-------------------TAAAAACACTT
|-||-|||-| | |||||||| |||||||||                      |||| ||
GTATCGTATTCCGAAGAATACCAACTACTTCTGCCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAAAC
1190      1200      1210      1220      1230      1240      1250      1260

1250      1260      1270      1280      1290      1300      1310
CTTCTAAC-------GGTTGCTTCTGGTCTTCATCTGTTCATCTAAAGAACACGGTTGGCAGGAAAACTAAGAAT
|-|-|||        |||||| |||||| ||||||-|||||| -||||| ||
CGTACAACCTGAAACTGGGTTGCAATTGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTC
1270      1280      1290      1300      1310      1320      1330

X
TC
|
TAGAGTCGAGGCCTGCAG
X 1340    1350
```

```
> O <
O|O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-33-inv.res made by bobryen on Thu 7 Nov 102 14:51:42-PST.

Query sequence being compared:US-09-910-186A-33' (1-1314)
Number of sequences searched:                     3
Number of scores above cutoff:                    3

Results of the initial comparison of US-09-910-186A-33' (1-1314) with:
        File :US08123975A.seq
```

Complement (handwritten annotation)

```
100-
    |
  N |
  U |
50- |
  M |
  B |
  E |
  R |
10- |
  O |
  F |
   5-|
  S |
  E |
  Q |
  U |
  E |
  N |
  C |
  E |
  S 0-|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
SCORE  0    4    7   11   15   18   21   22   26   29   33
               |    |    |    |    |    |    |    |    |    |
STDEV -8   -7   -6   -5   -4   -3   -2   -1    0
```

```
                PARAMETERS

Similarity matrix    Unitary
Mismatch penalty     1
Gap penalty          5.00
Gap size penalty     0.33
Cutoff score         1
Randomization group  0

              SEARCH STATISTICS

Scores:         Mean      Median    Standard Deviation
                 31         28            3.46

                 CPU                  Total Elapsed
Times:       00:00:00.00              00:00:00.00

Number of residues:                  4027
Number of sequences searched:           3
Number of scores above cutoff:          3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                                        Init. Opt.
Sequence Name     Description                              Length  Score Score  Sig. Frame
-------------     -----------                              ------  ----- -----  ---- -----
1. US-08-123-975A-4  Sequence 4, Application U             1338    33   462   0.58    0
2. US-08-123-975A-1  Sequence 1, Application U             1338    33   462   0.58    0
                     **** 1 standard deviation below mean ****
3. US-08-123-975A-6  Sequence 6, Application U             1351    27   458  -1.15    0
```

```
1. US-09-910-186A-33' (1-1314)
   US-08-123-975A-4  Sequence 4, Application US/08123975A

Initial Score    =    33   Optimized Score =    462   Significance =   0.58
Residue Identity =    41%  Matches         =    560   Mismatches   =   711
Gaps             =    91   Conservative Substitutions =    0
```

```
         x         10        20        30        40        50        60
         GAATTCTTAGTTTCCTGCCAACCGTGTTCTTTAGAGATGAAAGACCAGAAGCAACCGTTAGAAGA
         ||    ||||| |||  ||||| | ||| |||  ||||   ||| ||||| || ||| |||||||||
         CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCAATACCTCCATCCTGA
    x 10        20        30        40        50        60        70

         70        80        90        100       110       120       130
         AGTGTTTTACGGATGTGTTGGAGTACCATGAAGAAGAAGCAACCAGGTTGTTAGAGTGGAAACCCAGCA----
         |  || || ||  |||||  ||||  |||||||| |  || ||||||| |   ||  ||| |||  ||
         ACCTGGCTACGAA------TCCAATCACCTGATCGACCTGTCTCG--CTACGCTTCCAAAATCAACATCGG
    x    80        90        100       110       120       130

         140       150       160       170       180       190       200
         GACCGATGTTACCACCGTGTTGTTCTGGAAGTTCATAGTGCAGTTGTTACCGATGGAGTCCATAACGAT-G
         || | ||||||| | | ||| |  | |||||  || ||||| || |   ||||  |||| ||| |||| |
         TTCTAAAGTTAACTTCGAT-CCGATCGACAAGAATCAGATCCAGCTGTTCAATCTCGGAATCTTCCAAAATCG
    x    140       150       160       170       180       190       200

         210       220       230       240       250       260       270
         ATCTGACCCAGAGAGTTGTTAGAGTTAGAAGTACGGATCAGTTTGATGATTTTTCCGGTTTAGCGATAGAG---
         | || |  | | || ||| | ||  |  |||  ||| || |  || |  | ||  | ||   | ||  ||
         AAGTTATCCTGAAGAATGCTATCGT--ATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTCGA---
    x    210       220       230       240       250       260       270

         280       290       300       310       320       330       340
         ATGTCAGGCTACAGACGGTATTCAACGTCACGGTCAACAACGTTGATGTAAGCCAGGTCGTTTTTACGTACG
         |  | |  ||   |  ||  || |  |||| ||   |  ||  ||||| ||||| | | | || ||| |||||
         ---TCCGTATCCCGAAAATACTTCAACTCCATCTCTGAACAATGAATACACCCATCATCAACTGCATGGAAA
    x    280       290       300       310       320       330       340

         350       360       370       380       390       400       410
         A-AGTTGTCAGTGTTAGATGTCAGTAGAACCGTTTTACGGATAGAACTTCAACAC---CAGTGTACAG
         |  ||||| ||  | |||  || ||||| ||| | |||| || | ||||| | ||      ||| ||
         ACAATTCTGGTTGGAAGTATCTCGACTACGGTGAAATCATCTCGACTCTGCAGGACACTCAGGAAATCA
    x    350       360       370       380       390       400       410

         420       430       440       450       460       470       480
         ACGAGTGTTAGAGAAGAGATATTAGGTTTCGTAATAAACACCA-CGCTG-CTGGTTGATGTTCAGGAAGTTAGAG
         ||| | | |  ||| | |  || || || ||    |||  ||| |     | |  ||||| || | | ||| |||
         AACAGCGTGTTGTATTCAAATA-CTCTCAGATGATCAACATCTCTGACTACTCAACAATCGTCTGGATCTTCGTT
    x    420       430       440       450       460       470       480

         490       500       510       520       530       540       550
         TTCTGAGTGATAGATTTGTCAGTCCGGACAGGTTCAGCAGGTTAGTAACGTTTGTTGTAC----AGCAGGTA
         ||| |  || | ||| ||| ||  || | || |||| ||||  ||| |  || || ||||       ||||| |
         ACCATCACCAACAACATCGTCTGAATAACTCACATCTCCAAAATCTACATCACCGCCGTCGATGACCAGAAACCGATC
    x    490       500       510       520       530       540       550

         560       570       580       590       600       610       620
         GTTACCCCAGAAGTCTTCAGGATGACGGGTCCGGTTCGTCGACGTAGACAGAGTTTCGATTTCAGTTTACC
         |||  | | | ||| | | || | || | |  || |||| | | || | || | ||| || | |  |||
         TCCAATCTGGGTAACATCCACGCTTCTAATAACATCATCATGTCAAACTGGAGACTGGACGGTTGTCGTCGACACTCACCGC
    x    560       570       580       590       600       610       620

         630       640       650       660       670       680       690
         CAGTTCAGTGTCGAAAACTTGAGTAACGAACGTACCACGTAACGCCGTCGTTCGCAACCAACGATTT----
         |  ||| |||| ||   ||||| |||||  ||  |  ||| | ||||||    |||
```

TACATCTGGATCAAATACTTCAATCTGTTCGA---CAAAGAACTGAACGAACGAAAAGAAATCAAAGACCTGTAC
630   650   660   670   680   690

--TGAACAGGAGGATGTGTCAGAAACGTGGGATGTAGAGATAGATTTTCATCGATCAGGTTACC
700   710   720   730   740   750   760
GACAACCAGTCCAATCTGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGAACCGTACTAC
700   710   720   730   740   750   760   770

GTTGATGTAGATACGAGAGAGTTGTTACCCAGACGGTTGTTAGTGATAGTAACGAAG--ATCCATTTATTAATGTAG
770   780   790   800   810   820   830
AT--GCTGAATCGTACGATCCGAACAAATACGTGCAGTATCCGCGGTTACATGTA-
770   780   790   800   810   820   830

TCAGAGATAGAGATCATCTGAGTGTAGT--TGAAAACCAGTTTCTGGTTGTTACCCAGCTGTCCTGCAGAG
840   850   860   870   880   890   900
AT--GCTGAATCGTGACGATCCGAACAAATACGTGACTGTTGTTACGTGATCCCGTGTTTCCCGTACCGTGGTA
840   850   860   870   880   890   900

----CCTGGAAAGGTCCGCGTGGTGTTCTGTTGTTATGACTACCAACACTACCTGAACTCTTCCCTGACTGATCG
910   920   930   940   950   960   970
TCCAGATGATTTGTTGTTAGTTCAGAGAGATTTCCAACCAGAGTTGTTACGGATGCAGTCGATGATAG
910   920   930   940   950   960   970

CCAAATTCATCATCAAGAA----ATACGCGTTCTGGTAACAAG---GACAAATATCGTTCGCAACAATGATCG
980   990   1000   1010   1020   1030   1040
TGTAT---TCGTTGTTCAGTTAACTTTGTTGAAGTATTTCGGGATACGAA-----CCCAGAAAGAGAGATAGA
980   990   1000   1010   1020   1030   1040

GAAGTTCACGATGTGGT-AACGACCGTTGAGATGATGTCGTTGTTCTGAGCGATGTTACTTCAGACGGTTTAGAAG
1050   1060   1070   1080   1090   1100   1110
TGTATACATCAATGTGTAGTTAAGAACAAAGAATCACGTCTGCGTCTACCAATGCTTCAGCGTGGTGTGA
1050   1060   1070   1080   1090   1100   1110

AAAGATCTTGTCTGCTCTGCGAAAATCCCGGACGTTGGTAATCGTTGGTAATCCTGTCTCGG--TAGTTGTAATGAAATCCAAG
1120   1130   1140   1150   1160   1170   1180
AGTAGATCCGAACTGGTTGCGGTTGGTTTTGAGTAGATGTAGAGATGGTAGAGACGTTGAGATAGAGATGTTAGAACCAT
1120   1130   1140   1150   1160   1170   1180

AG---------CCAGAGATGTCGGATGAATTTGTTGTTTC--GTAACGGCATGTCCAGGATAGAGTTGGTC
1190   1200   1210   1220   1230   1240
AACGACCAGGGTATCACTAACAAAT-GCAAAATGAAATCTGCAGGACAACAATGGTAACGATATCCGGTTTCAT
1190   1200   1210   1220   1230   1240   1250
CGGTTCCACCAGTTCAACAATATGCTAAACTGGTTGCTTCCAACTGGTACAACATCGATCGAACCGTTC

TTTGATTTTTTGTACAGTTGTTGTTGAGTACAGGATCAGGATTTTGTCGTTAGTGTAAGACAACGTGAATTC
1250   1260   1270   1280   1290   1300   1310   X
CTCTCGCACTCTGGGGTGCTCTGGGAGTTCA--TCCCGGTTGATGACGGTTGGGGTGAACGTCCGGCTGTAA
1260   1270   1280   1290   1300   1310   1320   X

CCCGGGAAAGCTT
1330

2. US-09-910-186A-33' (1-1314)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score   = 33   Optimized Score   = 462   Significance = 0.58
Residue Identity = 418   Matches   = 560   Mismatches   = 711
Gaps   = 91   Conservative Substitutions   =   0

X   60
GAATTCTTAGTTTTCCTGCCAACCGTGTCTTTTAGAGATGAAAGACCAGAAGCAACCGTTAGAAGA
X 10   20   30   40   50   60   70

AGTGTTTTACGGATGTTGTTGTGTAGTACCAGGAAGAGCAACCAGGTTGTTGAGTGGAAACCCAGCA---
70   80   90   100   110   120   130
ACCTGCGTACGAA------TCCAATCACCTGATCGAACGTCTCG--CTACGCTTCCAAATCAACATCGG
70   80   90   100   110   120   130

GACCGATGTTACCACCGTGTTGTTCTTGGAAGTTCATAGTGCAGTTGTTACCGATGAGTCGTTAACGATCG
140   150   160   170   180   190   200
TTCTAAAGTTAACTTCGAT-CCGATCGACACGAGATCCAGCGTGTCAATCTGGAATCTTCCAAAATCG
140   150   160   170   180   190   200

ATCTCACCCAGAGAGTGTTGATTCAGTTGGATACGGATCAGTTTGATGATTTTTCCGGTTTAGCGGATAGAG
210   220   230   240   250   260   270
AAGTTATCCTGAGAAGTCTATCGT---ATACAACTCTATGTACGAAAAACTCTGAACTCTTCTGGA---
210   220   230   240   250   260   270

ATGTCAGGTACAGACGGTATCAACGTCACGGTCAACAACGTTCAGTGATGTAAGCCAGGTCGTTTTACGTACG
280   290   300   310   320   330   340
---TCGTATCCCGAAATACTTCAACTCATCTCTGACAATGATCTGACAATGCATCATCAACTGCATGAAA
280   290   300   310   320   330   340

A-AGTGTCAGTGTTAGAGATGTCAGTAGAACCGTTTTACGGATAGAACACAC---CAGTGTACAG
350   360   370   380   390   400   410
ACAATTCGTGTTGGAAAGTATCTCTGAAATCATCTGGACTCTGCGAGGACTCAGGAAATCA
350   360   370   380   390   400   410

ACGGATGCTTAGAAGAAGATATTAGGTTTCTGATAAACACCA-CGCTG-CTGGTTGATGTTCAGGGAAGTTAGAG
420   430   440   450   460   470   480
AACAGCGTGTTGATTCAAATA-CTCTCAGATGCATCAACATCTGACTACAATCGCTCTGGATCTTCGTT
420   430   440   450   460   470   480

TTCTGCAGTAGATATTGTGTTCCGGAGCCAGGTTCAGCGGGAGTAACGTTTGTTGTAC----AGCAGGTA
490   500   510   520   530   540   550
ACCATCACCACCAACATCGTCTGAATAACTCCAAAATCTACATTCACGGCGTCGATCGATCGACCAGAAACCGATC
490   500   510   520   530   540   550

GTTACCCCGAGAGTCTTTCAGGATAGACGGGTCCGGTTCGTCAGAGTACAGAGTTCGATTTCAGTTTTACC
560   570   580   590   600   610   620
TCCAATCTGGGTAACGATCCACGCTTCTAATAACTCGTTCGA--CAAAGAACTACTGGACGGTTGTCGTTGCAACACTCACCGC
560   570   580   590   600   610   620

CAGTTCAGTGTCGAAAACTTTGAAGTACGGATAACCAAGCGTAACGGGTCGTCGTTGTTGCAACCAACGGATTT----
630   640   650   660   670   680   690
TACACTCTGGATCAAATATGATCAATCTGTTCGA---CAAAGAACTGAACGAACGTGTAGATAGAAGCCGTACTAC
630   640   650   660   670   680   690

GTTGATGTAGATACGAGAGAGTTAGTGATGTAGTGATAACGAAG--ATCCATTTATTAATGTAG
700   710   720   730   740   750   760
GACAACCAGTCCAATCTGTATCCTGAAAGACTTCGGGGTGACTACCTGCAGTACGAACCGTACTAC
700   710   720   730   740   750   760   770

AT--GCTGAATCGTGACGATCCGAACAAATGCGTGTTACGTGATCCCGTGTTTCCCGTACCGTGGTA
770   780   790   800   810   820   830
GTTGATGTAGATACGAGAGAGTTGTTACCCAGACGGTTGTTAGTGATAGTAACGAAG--ATCCATTTATTAATGTAG
770   780   790   800   810   820   830

TCAGAGATAGAGATCATCTGAGTGTAGT--TGAAAACCAGTTTCTGGTTGTTACCCAGCTGTCCTGCAGAG
840   850   860   870   880   890   900
----CCTGGAAAGGTCCGCGTGGTGTTCTGTTGTTATGACTACCAACACTACCTGAACTCTTCCCTGACTGATCG
840   850   860   870   880   890   900

(continued alignment data)

3. US-09-910-186a-33' (1-1314)
    US-08-123-975A-6 Sequence 6, Application US/08123975A

```
Initial Score       =   27     Optimized Score        =  458     Significance  = -1.15
Residue Identity     =   40%    Matches                =  553     Mismatches    =  727
Gaps                 =   102    Conservative Substitutions
```

[Sequence alignment of nucleotide sequences with position numbering from ~10 to ~1330, displaying aligned DNA sequences with match bars. The alignment continues across two columns of the page.]

```
       TTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGT-AT
       1130      1140      1150      1160      1170      1180      1190

       1170      1180      1190      1200        1210      1220
       AGAGATGTTAGAACCATAGCCAGAGATGTCGAT-------GAATTTGTTGTTTTCGTAACGCA---TGTC
         -  | | |||||  |  |||  |   ||  |        |||||  ||
       CGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTAACCTGAGGAAGTTAAAACGCAAAACCGTA
       1200      1210      1220      1230      1240      1250      1260

       1230      1240      1250      1260      1270      1280      1290
       CAGGATAGAGTTGTCTTGATTTTTTTGTACAGTTTGTTGAAGTACAGGATCAGGATTTTGTCGTTAGTGTA
       ||  -|  || || |||   ||  | ||     ||  ||    |||||  |||  ||
       CAACCTGAAACTGGGTTGCAATTGGCAGTTCA---TCCCGAAAGACGAAGGTTGACCGAATAGTAACCTCT
       1270      1280      1290      1300      1310      1320      1330

       1300    1310    X
       AGACATCGTGAATTC
       |||  ||| -|
       AGAGTCGAGGCCTGCAG
       1340      1350
```

```
> O <
O| |O  Intelligenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-34.res made by bobryen on Thu 7 Nov 102 14:38:25-PST.

Query sequence being compared:US-09-910-186A-34 (1-432)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-910-186A-34 (1-432) with:
        File :US08123975A.pep)

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
			**** 1 standard deviation above mean ****			
1.	US-08-123-975A-2 Sequence 2, Application U	850	208	264	1.14	0
		**** 0 standard deviation from mean ****				
2.	US-08-123-975A-3 Sequence 3, Application U	415	171	296	-0.42	0
3.	US-08-123-975A-5 Sequence 5, Application U	439	164	256	-0.72	0

1. US-09-910-186A-34 (1-432)
    US-08-123-975A-2 Sequence 2, Application US/08123975A

```
Initial Score      =   208      Optimized Score      =   264    Significance =    1.14
Residue Identity   =   35%      Matches              =   163    Mismatches   =   231
Gaps               =   28       Conservative Substitutions    =    33

                    x        10        20        30        40        50
          MSYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVY
          ||||| ||  || :| ||||||| || :| || ||||:: |:|||:|  ||
AEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVE
380         390       400       410       420       430       440       450

                    60        70        80        90       100       110       120
IYSTNRNQFGIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKV---NLNNEYTIIDCIRMNNSG
 |||  |||| |||||||||||:| ||:  :  ||:||: |||||   ||||     |||||||| || |||
L--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMK-NNSG
460         470       480       490       500       510       520

                    130       140       150       160       170       180       190
WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIIDEKSISNLG
||||  :|||||| ||    |||||| | :  ||||||: |||| | ||:|||||:|||||| |
WKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIR
530         540       550       560       570       580       590

                    200       210       220       230       240       250       260
DIHVSDNLFKIVGCND-TRYVGIRFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL
 ::  |||||| |    || |||| :|   :|| | ||  |   |: | :| ||||  | ||| |  :: *
EVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAG
600         610       620       630       640       650       660

                    270       280       290       300       310       320       330
RTDKSITQNSNF-LNINQQRGVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDV
 | |: | |||| |||:| |||:|||||||||:|||||| |:||||||||:||::||||||:|||  |||:||
NKNSYIKLKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ
670         680       690       700       710       720       730

                    340       350       360       370       380       390
EYRLYADISIAKPEKIKLLIRTSNSNSLGQIIVMD-----SIGNNCTMNFQNNNGGNIGLLGFH------
 | |  || || :| |  |: : |  ||   :| :     ||  |  :|| :
EWRVYTYKYFKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDESTDEIGLGIHRFYESGI
740         750       760       770       780       790       800

                    400       410       420            x
----SNNLVASSWYYNNIRKN--TSSNGCFWSFISKEHGWQEN
    | :| :| ||||  ||:|  |::|| || || ||| ||
VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
810         820       830       840       850
```

2. US-09-910-186A-34 (1-432)
    US-08-123-975A-3 Sequence 3, Application US/08123975A

```
Initial Score      =   171      Optimized Score      =   296    Significance =   -0.42
Residue Identity   =   49%      Matches              =   205    Mismatches   =   168
Gaps               =   17       Conservative Substitutions    =    27

          10        20        30        40        50        60        70        80
LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKPSEVNIAQNNDII
||| ||| |  ||| |||:  || ::| || |||||||| |||||:
RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
x        10        20        30        40        50
```

```
                    *
|           |           |           |           |  *   *    |208
|           |           |           |           |162 |185   |  1
|           |           |           |116  |139   | -1  |  0
|       |69  |92  |     | -2  |  -3
|46  |   | -4
|23  | -5
| -6
0-----|-------|-------|-------|-------|-------|-------|-------|-------|

SCORE  0|  -1  46  69   92   116   139   162   185   208
STDEV  -7  -6   -5   -4   -3    -2    -1     0     1
```

```
PARAMETERS

Similarity matrix      PAM-150        K-tuple                    1
Threshold level of sim.   16%         Joining penalty            3
Mismatch penalty       1              Window size               20
Gap penalty            5.00                                     432
Gap size penalty       0.05
Cutoff score           1
Randomization group    0

              SEARCH STATISTICS

           Mean      Median      Standard Deviation
Scores:    181       165         23.64

           CPU                   Total Elapsed
Times:     00:00:00.00           00:00:00.00

Number of residues:                  1704
Number of sequences searched:           3
Number of scores above cutoff:          3
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
         280       290       300       310       320       330       340
                                                                         410
                                                              -----SNNLVASWYYNNIR
                                   380       390       400         ::|  ||   ||
        360       370   ----SIGNNCTMNFQNNNGGNIGLLGFH--------------   |:: ||
RTSNSNNSLGQIIVMD                                390
        360       370       380
PISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLLIGIHRPYESGIVFEEYKDYFCISKWYLKEVK
        350       360       370       380       390       400       410

                                420       430
                  KN--TSSNGCFWSFISKEHGWQEN
                  :||:||:||||:||::|||||:|
                  RKPYNLKLGCNWQFIPKDEGWTE
                  420       430       X
```

3. US-09-910-186A-34 (1-432)
    US-08-123-975A-5 Sequence 5, Application US/08123975A

```
Initial Score    =     164   Optimized Score  =     256   Significance = -0.72
Residue Identity =     35%   Matches          =     156   Mismatches   =    226
Gaps             =     28    Conservative Substitutions  =      33
```

```
         10 X       20        30        40        50        60        70
MSYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKPSEVN
          |||  | ||    |:::|||:: |: |     |||::|
       FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIR
       X        10        20        30        40        50

         80        90       100       110       120       130       140
IAQNNDIIYNGRYQNFSISFWVRIPKYFNKV---NLNNEYTIIDCIRNNNSGWKISLNYNKIIWTLQDTAGN
     :| ||:  |  |||| ||||||||||| |      ||||||:||||:|:  |:||||||::||||
VTQONQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMK-NNSGWKISIRGNRIIWTLIDINGK
 60        70        80        90       100       110       120

        150       160       170       180       190       200       210
NQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIVGCND-TR
          | | ||:||||||||||  || :||| |:|||||::|| |  ||:|||||||||||:| |
TKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRIQ
130       140       150       160       170       180       190       200

        220       230       240       250       260       270       280
YVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNF-LNINQQR
:| ::| |||  ||:| |||:||||||||||:||||||||||||||||||||||||||||||| | ||||
FIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILIR
210       220       230       240       250       260       270       280

        290       300       310       320       330       340       350
GVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLI
:: :|| |||   | | ||:||  ||||:|   ||::  |  ||  |   ||:||:  |   ::||  |:||
SKYNQNSKYINYRDLYIGEKFIHRKSNSQSINDDIVRKEDYILYLDFFNLNQEWRYYTYKYFKKEEKLFLA
290       300       310       320       330       340       350

        430 X
GWQEN
|  |
GWGERPL
410 X
```